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BE654876 UI-M-BHO-
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ALIGNMENTS

PUBMED REFERENCE VERSION KEYWORDS RESULT AK020909 REFERENCE REFERENCE SOURCE DEFINITION ACCESSION Locus AUTHORS TITLE TITLE TITLE MEDLINE MEDLINE ORGANISM JOURNAL AUTHORS JOURNAL JOURNAL AUTHORS PUBMED Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930030D13:tumor necrosis factor (ligand) superfamily, member 12, full insert sequence. Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayshizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new components of the control o Meth. En: 99279253 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus musculus (strain:C57BL/6J) adult retina cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library Mus musculus HTC; CAP trapper. 11042159 20499374 clone: A930030D13. AK020909.1 GI:12861640 10349636 (sites) (sites) (sites) genes Mus

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REFERENCE
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                 gratefully acknowledged by Stefano Gustincich (Department Retina RNA was provided by Stefano Gustincich (Department Neurobiology, Harvard Medical School, 220 Longwood Ave., E 02115, USA) whose assistance is gratefully acknowledged.
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/strain="C57BL/6J"
/db_xref="MGD:MGI:1911867"
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                                tumor necrosis factor (ligand)
                                                                                                                                                                     /tissue_type="retina"
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                                                                                                                                                                                                                                                                                              Location/Qualifiers
                /codon_start=2
                                                                              /note="data
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http://image.llnl.gov
Plate: LLAM9767 row: p column: 20
High quality sequence start: 17
High quality sequence stop: 724.
Location/Qualifiers
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
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/db_xref="taxon:10090"
/clone="IMAGE:4206595"
/clone=Lib="NCI_CGAP_CO24"
/clone_Lib="NCI_CGAP_CO24"
/clone_Lib="NCI_CGAP_CO24"
/clone="Topin: Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 292 c 268 g 204 t 1 others
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/strain="FVB/N"
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                                                                                                                                                                                                                                                                                    Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov b column: 07 High quality sequence stop: 728.
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National Institutes of Health, Mammalian
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                    125
            /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5405478"
/clone_lib="NH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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604; Conser
                                                                                                                                                                           mRNA sequence.
B1870393
B1870393.1 GI:
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 728)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
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603395641F1 NIH_MGC_90
                                                                                                                                                    human.
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     Preparation: Life Technologies, Inc. Arrayed by: The I.M.A.G.E. Consortium
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12034 row: a column: 12
High quality sequence stop: 728.
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5405459"
/clone_lib="NHI_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
25 a 240 c 227 g 136 t
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Pred. No. 4.2e-113;
0; Mismatches 86;
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cttggaacaactagtccggcctcgaagaagtgctcctaaaggccggaaggcgcggcctcg
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                                                                                                                                                                                                                               GGTGCTGAGCCTGGGCCTGGCCTGGCCTTGGCCTCCTGGTCGTCGTCAGCCT 116
                                                              CCGCCGGGAGCCCCCTGAACTGAATCCCCAGACAGAGGAAAGCCAGGATGTGGTACCTTT
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                                                                                                                                                                                                                                                                                                                     504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Other_ESTs: ur70d09.x1
Contact: Robert Strausberg, Ph.D.
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ur70d09.yl NCI_CGAP_Mam3 Mus
similar to TR:054907 054907 :
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High quality sequence stop: 433
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="129 - C57/B6 - FVBN"
/db_xref="taxon:10090"
/clone="IMAGE:3155633"
/clone_iib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                        inote "Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetic 22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                                    43.2%;
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Pred. No. 2.6e-112;
0; Mismatches 1;
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This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
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Contact: Robert Strausberg, Ph.D.
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BE628951
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           /note-"vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                  /clone_lib="Soares_mammary_gland_NMLMG"
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                                                                                                                                                                                 /lab_host="DH10B"
                                                                                                                                                                                                  tissue_type="mammary gland"
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                                                                                                                                                                                                                                                                           /db_xref="taxon:
                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
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Query Match Best Local Matches 53

Local Similarity 99. mes 530; Conservative

42.68;

Score 497; DB Pred. No. 1.3e 0; Mismatches

DB 10; .3e-110;

Length 533; Indels

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                                                                                                        cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAMI0435 row: h column: 15 High quality sequence stop: 468.
                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                            BG404836 650 bp m 602420160F1 NIH_MGC_94 Mus musculus
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/Clone="IMAGE:4527038"
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/lab_host="DH108 (phage-resistant)"
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                                                            /organism="Mus musculus"
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                                                                                                                                                                                                     AW917574 584 bp mF EST3.88878 Rat gene index, normalized Rattus norvegicus cDNA clone RGIEF49 AW917574 GI:8083328 EST.
                                              Le (bases 1 to 584)
Le N.H., Glodek,A., Chandra,I.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of
                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                     Norway rat.
Rattus norvegicus
            Unpublished
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50; Conservative
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a 194 c 149 g 150 t
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Pred. No. 8.9e
0; Mismatches
                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                  of
                                                                                Mason, T.M.,
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}.9e-109;
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at, norvegicus, l'
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                                                                                Quackenbush, J.,
                                                                                                                                                                                                                                                         mRNA sequence
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                                                                                                                                                                                                    TCCCAGGTTCTTTAAACTNTAACCTAACAGCTCCCAGAGCACCACAGCACCTCCCCACCC
                                                                                                                                                                                                                                                            AAGGCTGCCCCTTCCTTACCTACTTTGGACTCTNTCAAGTTCACTGAGGGGTCCTGCTC
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BI819200
603034614F1 NIH_MGC_115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nhlee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information
Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (301)-838-3529
(301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBlueScript SK(-); Site_1:
Xho1; Estimated insert size approx.1 kb"
188 c 147 g 138 t 3 others
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Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver, embryo, heart,
/lab_host="SOLR"
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/db_xref="taxon:10116"
/clone="RGIEF49"
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liver, embryo, heart, muscle, spleen"
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Pred. No. 9.7e-107;
0; Mismatches 46;
 777 bp mRNA linear EST 04-OCT-2001 Homo sapiens cDNA clone IMAGE:5175698 5',
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                                                           tacctgtactgtcaggtgcactttgatgagggaaaggctgtctacctgaagctggacttg
                                                                                                                                   agccctctgcgctacgaccgccagattggggaatttacagtcatcagggctgggctctac
                                                                                                                                                                                                                                                                                                                                              GCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLMN1437 row: 1 column: 03 High quality sequence stop: 759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 777)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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BI819200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORR6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; and lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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/lab_host="DH10B"
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/clone="IMAGE:5175698"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 480.4; DB 10; Length 777; Pred. No. 1.7e-106; .
0; Mismatches 126; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by C.
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TITLE
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1 (bases 1 to 834)

NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
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Tissue Procurement: Life Technologies, Inc.
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Contact: Robert Strausberg, Ph.D.
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/note-"Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5206217"
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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National Institutes of Health, N
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/db_xref="taxon:9606"
/clone="IMAGE:5285892"
/clone=lib="NH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="PH10B"
/lab_host="PH10B"
/lab_host="PH10B"
/lab_host="ph10B"
/lab_host="ph10B"
/lab_host="ph10B"
/lab_host="hypothalamus"
/lab_host="hypoth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for full-length clones and constitutes of Health). Licenstructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Lil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
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Primates;
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Pred. No. 1.2e-100;
0; Mismatches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martli,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
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1 (bases 1 to 471)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:696209"
/clone_lib="Barstead mouse
                                                                                                                                                                                                                                            /sex="mixed"
                                                                                                                                                                                                                                                                                                                              /strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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Matches 457; Conserv
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rummalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 445)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

Waterston, R.
                                            Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:601556
                                                                                                                                                                                                                                                                                                                                            AA870722
445 bp mRNA li vq25g07.rl Barstead stromal cell line MPLRB8 clone IMAGE:1095324 5', mRNA sequence.
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Location/Qualifiers
1. .445
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Local Similarity 96.9 es 410; Conservative
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BE654876.1
EST.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 360)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                            BE654876 360 bp mRNA I
UI-M-BH0-ait-g-12-0-UI.rl NIH_BMAP_M_S1 Mus
UI-M-BH0-ait-g-12-0-UI 5', mRNA sequence.
                                                                         house mouse
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/db_xref="taxon:10090"
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96.5%;
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Pred. No. 1.1e
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No. 1.1e-84;
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   AI854476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse
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20892-9643, USA
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National Institute of Mental Health
National Institute of Mental Health
National Institute of Mental Health
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301 443 9890
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/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M.S1 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the
mouse brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hipoccampus). The driver used for
subtraction consisted of a pool of 20,000 cDNA clones
obtained from non-normalized and normalized libraries of
these ten regions of the mouse brain."

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/clone="UI-M-BH0-ait-g-12-0-UI"
/clone_lib="NIH_BMAP_M_S1"
/dev_stage="27-32 days"
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/strain="C57BL/6J"
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DEFINITION
345 CATTCCACAGACGTATCCTTGCTCTTCTTTAACATCCCATCCCACCACCAACTATCCACCT
                                              774 gctccttggtccagtcctgt-ctctcctcaaaggcagcagagcttgttcacatg-tttc 831
                                                                                                                                                                                              405 GCTCCTTGGTCCAGTCCTGTCCTCCTCAAAGGCAGCCAGAGCTTGTTCACATGTTTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UI-M-BH0-ait-g-12-0-UI.s1 NIH_BMAP_M_S1 Mus musculus cDNA clone UI-M_BH0-ait-g-12-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone_lib="NIH_BMAP_M_SI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_SI library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,000 cDNA clones of the subtraction consisted of a pool of 20,
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/strain="C57BL/6J"
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Dearch completed: June 22, 2002, 10:48:59 Job time: 18054 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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ALIGNMENTS

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RESULT
AAV18599
 18-MAR-1997;
07-AUG-1996;
18-OCT-1996;
                                                                                                                                                                            TRELL; tumour necrosis factor related ligand; tnf; treatment; cancer; autoimmune disease; immune system; stimulation; suppression; graft rejection; ds.
                                                       07-AUG-1997;
                                                                                          W09805783-A1
                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                Mus musculus tumour necrosis factor related ligand (TRELL) gene
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                                                                                                                                                                                                                                                      AAV18599;
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GENEVA FACULTY MEDICINE

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cc rigand (TRELL). TRELL or active fragments can be included with a CC diseases or immune responses to tissue grafts, or to stimulate or CC suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening CC compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon- gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human CC adenocarcinoma cells) involving a signal pathway between TRELL and its CC TRELL-related disorders in mammals (especially involving a utolumune and inflammatory diseases or inherited genetic disorders, CC by introducing into cells, and expressing, therapeutically effective CC amounts of a vector, e.g. a virus comprising a gene encoding TRELL. CC It may also be of use in the preparation of prepare probes for CC and for antisense therapy.
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28-APR-1999;
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20-JUL-1999;
26-JUL-1999;
15-SEP-1999;
15-SEP-1999;
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P-PSDB; AAY95338.
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08-MAR-1999;
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Novel composition to

inhibit neoplastic cell growth or

for treating

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The present sequence is that of cDNA clone DNA30879-1152 (ANTCC 209358) encoding human PRO207 (see AAY95338), which shows to homology to several members of the tumour necrosis factor family, especially human lymphotoxin (23.4%). The cDNA was identified in a feetal kidney cDNA library following identification of an expressed sequence tag with homology to human Apo-2 ligand. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO301, PRO207, PRO302, PRO219, PRO221, PRO224, PRO301, PRO526, PRO302, PRO330, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866 (see CAY95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, contain, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Nucleic acids encoding PRO179 etc. are used in the recombinant production of the antitumour polypeptides.
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PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509
PRO866 -
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10-OCT-1997;
                                                                                                                                                Homo
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                                                                                                                                                                                                                                                     AAX56000 standard;
        (GETH ) GENENTECH
                                                                                                                                                                                 Human; tumour
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                                                                                                                                                                        NF-kappaB-dependent transcription;
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related

(TRELL) gene

1357

1238 1023 1178

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968

936

SSXGG

837

897 721

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The sequence is that encoding human tumour necrosis factor related CC ligand (TRELL). TRELL or active fragments can be included with a CC carrier in pharmaceutical compositions to treat cancer, autoimmune CC diseases or immune responses to tissue grafts, or to stimulate or CC suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening CC compositions for binding. Agents interfering with TRELL-receptor CC binding can also be screened for, can then be administered, continuing the properties of alter immune responses (especially involving human CC adenocarcinoma cells) involving a signal pathway between TRELL and its creeptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. CC sord for anticase therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   responsive to TREPA and to screen for TREPA mimics. Ribozymes, antisense RNA, antibodies or peptides, are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting vascularisation), inflammation or a wide range of autoimmune conditions, conditions involving abnormal stimulation of epithelial cells (e.g. atherosclerosis), for birth control (inhibiting ovulation and placental formation) or other angiogenic conditions (e.g. ulcers).
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                   Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangictasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis; peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWEAK extracellular domain; tumour necrosis factor; TNF; anglogenesis; ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; ds;
                                                                                                                Wiley
                                                                           P-PSDB;
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Example 1;

Page

39-40;

46pp; English.

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CC pDC409-LZ-TWEAK, which encodes a fusion protein recording a growth CC hormone leader, a leucine zipper multimerisation domain, and the CC extracellular domain of human TWEAK. The fusion protein was used in the isolation of human TWEAK receptor (TWEAKR)-expressing clones CC from a COS cell human cDNA library. The TWEAK protein is a CI member of the tumour necrosis factor (TWE) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop CC angiogenesis. TWEAKR may therefore be used to screen for and develop CC used in the treatment and diagnosis of human disease. The disorders CC mediated by angiogenesis include coular disorders characterised by ocular CC retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, CC retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, CC retroscularisation, macular degeneration and corneal graft CC reumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.
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                                                                                                                                                                                                                      A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences in AAT19001-T28837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-c untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNA bybridise with specific mRNAS. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                              Query Match
Best Local Similarity
Matches 158; Conserv
1084
                                                         1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1067; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA tha reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene signature; messenger RNA; mRNA; relative abundance human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
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Qian F;
                                                                                                                                                                                                                              Antibodies (Ab) that distinguish between normal and mutant PKD1 sequences can also be used in diagnostic tests. Anti-PKD1 Ab may also be used to perform subcellular and histochemical localisation studies, and to block the function of PKD1. Ab are also useful in rational drug design studies to identify and test inhibitors of PKD1. Sense and antisense sequences derived from the PKD1 gene may
                                                                                                                                                                                                                                                                                                     The present sequence is the human polycystic kidney disease 1 (PKD1) gene. The PKD1 gene or polypeptide may be used to treat autosomal dominant polycystic kidney disease (APKD), and identify carriers of mutant PKD1 genes, i.e. subjects susceptible to APKD.
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autosomal dominant polycystic kidney disease; APKD;
                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Pages 90-118; 257pp; English.
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24-MAY-1996;
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The present sequence is that of the normal human PKDl gene from chromosome 16. Mutations in this gene (e.g. transitions, transversions, deletions and/or insertions) are associated with adult-onset polycystic kidney disease (APKD). The PKDl locus is GC-rich (62.4%). Comparison of this sequence with a previously reported partial cDNA sequence revealed differences at three locations (see features table). The most significant difference is the presence of two additional cytosine residues on the plus-strand at position 4566 of the previously reported sequence. The insertion
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(UYJO ) UNIV JOHNS HOPKINS.
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The present sequence is the human polycystic kidney disease 1 (PKD1) locus between chromosomal markers ATPL (ATP6C) and D16S84 The PKD1 gene or polypeptide may be used to treat autosomal
                                                                                                                                          Burn
Qian
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                                                                           Human polycystic kidney disease gene, PKD1 diagnose human autosomal or adult onset po
                                                                                                                                                                                                       03-JUN-1996;
24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                             Human; polycystic kidney disease 1; PKD1; treatment; autosomal dominant polycystic kidney disease; APKD;
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                                                   Example 5;
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                                                                                                                                                                                                                                                                      27-NOV-1997.
                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                               (GENZ ) GENZYME
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                                                                                                                                                                                                                                                                                                                                                                                     PKD1
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                                                   Pages 60-89;
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96US-0655360
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                                                                                                                                                                               CORP.
                                                                                                                                                      Η,
                                                                                                                                                                                                                                                                                                                                                                                   between chromosomal markers ATPL (ATP6C)
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                                                                                                                                                      Dackowski
                                                  257pp;
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                                                   English.
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                                                                            onset polycystic
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                                                                                        - useful to
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                                                                            disease
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Best Local S
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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Escobedo J,
Jones WL, K
Lamson G, L
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                                                                                                                                                                                                                                                                               Human; gene; gene expression product; diagnosis; therapy; detection; mapping; tissue typing; profiling; forensic; c genetic analysis; colorectal cancer; breast cancer; lung
                                                                                                                                                                                                                                                                                                                                Human gene expression product cDNA
                                     Crkvenjakov R,
                                                            (CHIR )
(HYSE-)
                                                                                                                                                                                                      05-AUG-1999
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                                                            ) CHIRON
) HYSEQ I
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v R, Dickson M, Drmanac
, Garcia PD, Garcia V,
Kassam A, Kennedy GC,
Leshkowitz D, Pot D, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%;
nilarity 48.7%;
Conservative
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                                                                                                98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
                                                                          CORP.
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   Drmanac R, Dr., Glese K, ... Kita D, I.
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Pred. No. 0.11
0; Mismatches
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RESULT 15
AAA02484/c
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Best Local
Matches 9
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                                                                       1321
                                                                                                                                              1261
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1337 BP;
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                                                                                                                                                                                                AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
CC libraries constructed from human colon cancer cell lines. The present
CC invention also describes a method of detecting differentially expressed
CC genes correlated with a cancerous state of a mammalian cell, comprising
CC detecting at least one differentially expressed gene product in a test
CC sample derived from a cell suspected of being cancerous, where detection
CC of the differentially expressed gene product is correlated with a
CC cancerous state of the cell from which the test sample was derived.
CC The polynucleotides sequences can be used in a method for detecting
CC differentially expressed genes correlated with a cancerous state of a
CC mammalian cell. The polynucleotides can also be used as probes for
CC detecting and mapping related genes. They can be used in diagnosis and
CC pre-metastatic or metastatic cancerous states, stages of cancer, or
CC responsiveness of cancer to therapy). This is particularly for breast
CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                            Query Match
Best Local
                                                                                             Matches
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15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
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(HYSE-)
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                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide library used to determine cancerous states
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                                                              689 ctctcccagattccttaaactttccctggctccaggagcatcaccacacctccctacccc
acceceactceteeaccecetegeteettggteeagteetgteteteeteaaaggea
                                         2000-126369/11
                                                                                            97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHIRON
HYSEQ I
                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 994; 1097pp; English
                                                                                                                                                               1000
                                                                                                                                                                                          breast cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer cell line
                                                                                             Conservative
                                                                                                                                                               BP;
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98US-0085537.
98US-0085696.
98US-0105234.
98US-0105877.
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                                                                                                          3.8%;
37.9%;
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Crkvenjakov R,
                                                                                                                                                               53
                                                                                                                                                                                         lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garcia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Innis MA,
                                                                                            Score 44.8; E
Pred. No. 0.05
0; Mismatches
                                                                                            0;
                                                                                                                                                                                          cancer,
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                                                                                                                                                               574
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                                                                                                                                                               G;
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v R, Dickson M,
Jones LW, Stac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; lung cancer;
                                                                                                                                                               22 T;
                                                                                                                                                                                          and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garcia PD,
                                                                                                            .054;
                                                                                                                      DB 21;
                                                                                                                                                               330
                                                                                             159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GC, Pot D, Kassam on M, Drmanac S, I Stache-Crain B;
                                                                                                                                                                                          cancer.
                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pot D, Ka
M, Drmanac
                                                                                             Indels
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Search completed: June 22, 2002, 11:53:24 Job time: $6741\ \text{sec}$

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Database sequences: 1736436
Database length: 858457221
Search time (sec): 287.880000
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Database: N_Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query: US-09-245-198A-2
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-DB=N_Geneseq_032802 -QFMT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QAPOP4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000-YGAPEXT=0.500
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -OHR -SCORE=pct
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US99245198_@CGN1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                line parameters:
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7.2e-84
7.6e-84
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0.5271
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seq_documentation_block:
ID AAV18599 standard; cDNA; 1168
XX
                                                                                                           The sequence is that encoding mouse tumour necrosis factor related CC ligand (TRELL). TRELL or active fragments can be included with a CC carrier in pharmaceutical compositions to treat cancer, autoimmune CC diseases or immune responses to tissue grafts, or to stimulate or CC suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening CC compositions for binding. Agents interfering with TRELL-receptor CC binding can also be screened for, can then be administered, optionally with interferon-gamma, to induce cell death or CC reat, suppress or alter immune responses (especially involving human CC adenocarcinoma cells) involving a signal pathway between TRELL and its Creeptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, CC autoimmune and inflammatory diseases or inherited genetic disorders, CC introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. CC It may also be of use in the preparation of prepare probes for creening natural/synthetic DNAs for TRELL-encoding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV18599
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:ABH20349
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH98231
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH98319
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07-AUG-1996;
18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Pages 45-46; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necrosis factor related ligand - useful for, cancer, auto-immune disease and immune responses to % \left( 1\right) =\left\{ 1\right\} =\left\{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-145619/13.
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                                                                                        for antisense therapy.
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UNIV GENEVA FACULTY MEDICINE.
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96US-0023541.
96US-0028515.
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Sequence 1168

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0 other;

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alignment_block:
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                                                                                                                       rTyrPheGlyLeuPheGlnValHis 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSe 117
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                                                                                                                                                                                                           ArgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPheLeuTh
                                                                                                                                                                                                                                                                                                                                             SLeuGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuA
                                                                                                                                                                                                                                                                                                                                                                                                             ValTyrLeuLysLeuAspLeuLeuValAsnGlyValLeuAlaLeuArgCy
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                                                                                                                                                                                                                                                           GTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCCAGGGTCTTCCCTT
                                                                                                                                                                                                                                                                                                                           CCTGGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGGGCCCCCAGCTCC
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Ratio: 5.164
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alignment_block:
                                                                                          alignment_scores:
                                                                                                                                                                            CC This invention describes isolated Tumor Necrosis Factor (TNF) family Cr receptor polypeptides: APO4, APO6, APO8 and APO9 or their active CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or CC their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic CC moiety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of CC agents to the polypeptide/active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC for agonists and antagonists by binding and observing the changer in APO4 CC activity. Effective pharmacological agents useful in diagnosis or CC treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4 CC activity. The method is performed in vivo or in vitro. APO polypeptides CC are all useful as immunogens for preparing antibodies. APO4 is also CC useful for diagnosis/treatment of developmental or gestational CC abnormalities. APO8 was transfected to human breast carcinoma cell line MCF-7, and induced apoptosis.
                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaudhary
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                                                                                                                                                  Sequence 701 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example VII; Fig 13B; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON.
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DB; AAW93591.
                                    Quality: 1089.00
Ratio: 5.186
nilarity: 99.526
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                                                                                                                                                139 A;
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Align seg 1/1

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AAX23425

from:

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US-09-245-198A-2 x AAX23425

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV4761;
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                                                           CDS
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                                                                                                                                                                                   TNF; endothelium proliferative agent; TREPA; wound healing; sue grafting; vascularisation; apoptosis; autoimmune; birth of the state of
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                                                                                                                                                                                         control
                                                                                                                                                                                                                     cancer;
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alignment_block: US-09-245-198A-2 x AAV47613

Percent

Length: Gaps: Identity:

224

88

Align seg 1/1 to: AAV47613

from:

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1236

2 LeuSerLeuGlyLeuAlaLeuAlaCysLeuGlyLeuLeuLeuValValVa CTGGGCCTGGGCCTGGCCTGGCCTCGGCCTCCTGCTGGCCGTGGT

125 18

35

76

luLeuThrAlaGluAspArgArgGluProProGluLeuAsnProGlnThr

AGCTGGTGGCAGAGGAGCCAGGACCCGTCGGAACTGAATCCCCCAGACA

176

35

52

GluGluSerGlnAspValValProPheLeuGluGlnLeuValArgProAr

83 225 51 175

275

276

8

gArgSerAlaProLysGlyArgLysAlaArgProArgArgAlaIleAlaA GAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCG

85

AAGAAGTGCACCTAAAAGGCCGGAAAAACACGGGCTCGAAGAGCGATCGCAG

85

laHisTyrGluValHisProArgProGlyGlnAspGlyAlaGlnAlaGly

101

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alignment_scores:
Quality: 1020.00
Ratio: 4.744
^****larity: 95.982
                                                                                                             The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, also to induce apoptosis for treating cancer and eliminating autoreactive T cells, as an adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can also be used to target cytotoxic agents or for affinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more responsive to TREPA and to screen for TREPA mimics.
                                                                                                                                       Ribozymes, antisense RNA, antibodies or peptides, are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting vascularisation), inflammation or a wide range of autoimmune conditions, conditions involving abnormal stimulation of epithelial cells (e.g. atherosclerosis), for birth control (inhibiting ovulation and placental formation) or other angiogenic conditions (e.g. ulcers).
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 123-4; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting nucleic acid encoding TREPA - useful for diagnosis treatment of autoimmune disease, tumours and inflammation
                                                                                                           Sequence 1236 BP; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW29745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-447255/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-1998;
12-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1998;
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97US-0798692.
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                                                                                                             Α,
                                                                                                             416
                                                                                                           Ç;
                                                                                                             358
                                                                                                             G;
                                                                                                           237
                                                                                                             Ŧ;
                                                                                                             0 other;
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ValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSe

375

GTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAG

425

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seq_documentation_block:
ID AAD04350 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576
                                                                                                                                                                                                                                                                                                     grafting; vulnerary; ss.
                                                                                                                                                                                                                                                                                                                Human; tumour necrosis factor; TNF; angiogenesis; wound healing;
TREPA; TNF related endothelium proliferative agent; tumour; meta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726
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             P-PSDB; AAE00891
                                                Wiley
                                                                                                                                   26-JUN-1998;
                                                                                                                                                           27-MAR-2001.
                                                                                                                                                                                 US6207642-B1
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                            04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                    AAD04350;
                                                                       (ABBO ) ABBOTT
                                                                                                12-FEB-1997;
10-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rPheGlyLeuPheGlnValHis 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 euCysGlnValSerGlyLeuLeuProLeuArgProGlySerSerLeuArg
|||||||||||||||||||||||
|TCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rProLeuArgTyrAspArgGlnIleGlyGluPheThrValIleArgAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCACCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGCCCTGCGCTGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCGGACTCTTCCAGGTTCAC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTG
                          2001-280760/29.
                                                  SR;
                                                                                                                                                                                                                                                                                                                                                    TREPA (TNF related endothelium proliferative
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                         LAB
                                                                                             97US-0798692
98US-0021706
                                                                                                                                   98US-0105343
                                                                                                                                                                                                    /*tag= a
/product= "Human TREPA (TNF related endothelium
proliferative agent)"
                                                                                                                                                                                                                                           Location/Qualifiers 1..750
                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA; 1236
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                                                                                                                                                                                                                                                                                                                                                    agent) cDNA.
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                                                                                                                                                                                                                                                                                                                  metastasis;
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Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain of tumor necrosis factor related endothelium proliferative agent protein
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Example 2; Column 73-74; 53pp; English.

Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing anglogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present sequence is a cDNA clone ID #690050 encoding human TREPA. The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent).

Sequence 1236 BP; 225 Α; 416 C; 358 G; 237 T; 0 other;

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alignment_scores:
    Quality: :
    Ratio:
    Percent Similarity:
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US-09-245-198A-2 x AAD04350
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                        168
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                                                                TyrLeuLysLeuAspLeuLeuValAsnGlyValLeuAlaLeuArgCysLe
                                                                                                                                                                                                           lSerLeuGlySerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluG
                uGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuArgL 185
                                                                                                                                                                                                                                                                                                                    AAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAG
                                                                                                                                                                                                                                                                                                                                  gArgSerAlaProLysGlyArgLysAlaArgProArgArgAlaIleAlaA
                                                                                                                                                                                                                                                                                                                                                                       GAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCG
                                                                                                                                                                                                                                                                                                                                                                                               GluGluSerGlnAspValValProPheLeuGluGlnLeuValArgProAr
                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTGGTGGCAGAGGAGGACCAGGACCCGTCGGAACTGAATCCCCAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   luLeuThrAlaGluAspArgArgGluProProGluLeuAsnProGlnThr
                                                                                                       GGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTC
                                                                                                                   lyLeuTyrTyrLeuTyrCysGlnValHisPheAspGluGlyLysAlaVal
                                                                                                                                                          CCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTG
                                                                                                                                                                        rProLeuArgTyrAspArgGlnIleGlyGluPheThrValIleArgAlaG
GGAGGAATTCTCAGCCACTGCGGCGAGTTCCCTCGGGCCCCAGCTCCGCC
                                                  TACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGCCCTGCGCTGCCT
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4.744
95.982
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Gaps: 0
Percent Identity: 88.839
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625
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seq_
   seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA49717
                                                                                                                                                                                                             22-DEC-1998

08-MAR-1999

21-APR-1999

28-APR-1999

14-MAY-1999

20-JUL-1999

26-JUL-1999

15-SEP-1999

15-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _documentation_block:
The present sequence is that of cDNA clone DNA30879-1152 (ATCC 209358) encoding human PRO207 (see AAY95338), which homology to several members of the tumour necrosis factor especially human lymphotoxin (23.4%). The cDNA was identi
                                                                                   Novel composition to inhibit neoplastic cell growth or tumor in mammal comprises polypeptides PRO179, PRO207, PRO221, PRO328, PRO301, PRO526, PRO362, PRO356,
                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breast cancer; uterine cancer
                                                                                                                                                          Ashkenazi AJ, Goddard
Napier MA, Pitti RM,
                                                                                                                                                                                                                                                                                                                      02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           central nervous
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                                                                                                                                                                                                                                                                                                                                           29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                WO200037638-A2
                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA49717 standard;
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                                                                                                                                                                                          (GETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rPheGlyLeuPheGlnValHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGG
                                                                                                                             2000-442668/38.
DB; AAY95338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO207
                                                     20;
                                                                                                                                                                                          GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA clone DNA30879-1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                     'n
                                                                                                                                                                                                             98US-0113296.
99WO-USO5028.
99WS-0130232.
99US-0131445.
99US-0134287.
99US-0144758.
99US-0145698.
99WO-US211990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovarian cancer; renal cancer; colorectal; prostate cancer; lung cancer; bladder casses system cancer; melanoma; leukaemia; neop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antitumour;
                                                                                                                                                                                                                                                                                                                      99WO-US28565
                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
58..177
/*tag= b
178..804
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 58..807
                                                    172pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA;
                                                                                                                                                            Wood
                                                    English.
                                                                                                                                                            Godowski PJ,
1 WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour; therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               747
                                                                                                                                                                     Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia; neoplasm; ss
                                                                                                                                                                     ÀL,
                                                                                                                                                                     Marsters
                                                                                   f for treating
PRO320, PRO21
PRO509 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
          shows family,
                                                                                   PRO219,
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alignment_block:
US-09-245-198A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foetal kidney cDNA library following identification of an expressed sequence tag with homology to human Apo-2 ligand. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO179, PRO207, PRO320, PRO221, PRO224, PRO230, PRO301, PRO36, PRO36, PRO356, PRO59 or PRO866 (see ARY95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Nucleic acids encoding PRO179 etc. are used in the recombinant production
                              185
                                                                                                                                                                                                                                                         483
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683
                                                              633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGG
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             euCysGlnValSerGlyLeuLeuProLeuArgProGlySerSerLeuArg
                                                                                                                                                                                                                                                         CCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gArgSerAlaProLysGlyArgLysAlaArgProArgArgAlaIleAlaA
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                                                                           uGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuArgL
                                                                                                                                           TyrLeuLysLeuAspLeuLeuValAsnGlyValLeuAlaLeuArgCysLe
                                                                                                                                                                                          GGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTC
                                                                                                                                                                                                         lyLeuTyrTyrLeuTyrCysGlnValHisPheAspGluGlyLysAlaVal
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                                                                                                                          TACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGCCCTGCCCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTGGTGGCAGAGGACCAGGACCCGTCGGAACTGAATCCCCAGACA
                                                            GGAGGAATTCTCAGCCACTGCGGCGAGTTCCCTCGGGCCCCAGCTCCGCC
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Identity:
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seq_documentation_block:
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                  diseases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for services of the preparation of prepare probes for services of the preparation of prepare probes for the preparation of the preparation of the prepa
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07-AUG-1996;
18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor related ligand - useful for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that encoding human tumour necrosis factor related ligand (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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graft rejection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV18600;
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P-PSDB; AAW47525.
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seq_documentation_block:
ID AAX56000 standard;

DNA; 1421 BP

seq_name:

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX56000

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alignment_block:
US-09-245-198A-2 x
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             rPheGlyLeuPheGlnValHis
                                                                  IleargThrLeuProTrpAlaHisLeuLysAlaAlaProPheLeuThrTy
                                                                                                                    euCysGlnValSerGlyLeuLeuProLeuArgProGlySerSerLeuArg
                                                                                                                                                           GAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCCCAGCTCCGCC
                                                                                                                                                                                     uGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuArgL
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                                                                                                                                                                                                                                                                                                                                                                                                  ValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSe
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                                                    ATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCACCTA
                                                                                                         TCTGCCAGGTGTCTGGGCCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGG
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alignment_scores:
Quality:
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US-09-245-198A-2 x
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                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                           217
                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human tumour necrosis factor (TNF) and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has cytostatic activity. Apo-3 ligand can be used to induce apoptosis in mammalian cancer cells, to induce NF-kappaB-dependent transcription amammalian cancer cells, to induce NF-kappaB-dependent transcription amammalian cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1998;
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10-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NF-kappaB-dependent transcription; JNK/SAPK-dependent response;
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                                                                                                                                                   LeuSerLeuGlyLeuAlaLeuAlaCysLeuGlyLeuLeuLeuValValValVa
            GluGluSerGlnAspValValProPheLeuGluGlnLeuValArgProAr 68
GAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCG
                                                                                                      lSerLeuGlySerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluG
                                                                                                                                       CTGGGCCTGGCCTGGCCTGCCTCGGCCTCCTGGCCGTGGT
                                                        luLeuThrAlaGluAspArgArgGluProProGluLeuAsnProGlnThr
                                                                                          CAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGG
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DB; AAY09369.
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97US-0062037
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/product= "Apo-3 ligand"
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seq_documentation_block:
ID AAS03964 standard;
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                                                                                                                                                              retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; ds; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis; peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;
                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 817
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                                                                                                              Synthetic
                                                                                                                                                                                                                                                                            ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
                                                                                                                                                                                                                                                                                             TWEAK extracellular domain; tumour necrosis factor; TNF; angiogenesis;
                                                                                                                                                                                                                                                                                                                       Expression vector pDC409-LZ-TWEAK fusion protein-encoding DNA.
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|CAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAG
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                                                                                                                                                     protein.
                                                   Location/Qualifiers 52..873 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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/*rag= a /product=

"Fusion protein comprising a growth hormone leader, a leucine zipper multimerisation domain, and human TWEAK extracellular

domain, domain

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alignment_block:
US-09-245-198A-2 x AAS03964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pDC409-LZ-TWEAK, which encodes a fusion protein comprising a growth hormone leader, a leucine zipper multimerisation domain, and the extracellular domain of human TWEAK. The fusion protein was used in the isolation of human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human cDNA library. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                        300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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10-MAY-2000;
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                                                 ArgSerAlaProLysGlyArgLysAlaArgProArgArgAlaIleAlaAl
                                                                                                                      GCTGGTGGCAGAGGACCAGGACCCGTCGGAACTGAATCCCCAGACAG
                                                                                                                                                    uLeuThrAlaGluAspArgArgGluProProGluLeuAsnProGlnThrG
                                                                                                                                                                                        AGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGA
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seq_documentation_block:
ID AAX23424 standard;
seq_name:
                                                                                                                                                        CDS
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                  (UNIW ) UNIV WASHINGTON
                                                               04-SEP-1998;
                                                                                                                                                                                                                apoptosis; human;
                                                                                                                                                                                                                                                                                 Human TNRL3 DNA.
                                                                                                                                                                                                                                                                                                        18-JUN-1999
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                                          05-SEP-1997;
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                                          97US-0924634
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/product= "TNRL3"
                                                                                                                                                        Location/Qualifiers
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CC This invention describes isolated Tumor Necrosis Factor (TNF) family Creceptor polypeptides: APO4, APO6, APO8 and APO9 or their active CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or CC their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic CC moiety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/ active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/ active fragments are also useful for screening CC activity. Effective pharmacological agents useful in diagnosis or CC treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational CC abnormalities. APO8 was transfected to human breast carcinoma cell line CC abnormalities. APO8 was transfected to human breast carcinoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and
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aAlaHisTyrGluValHisProArgProGlyGlnAspGlyAlaGlnAlaG
                                                                                                                                                                                                                          ArgArgSerAlaProLysGlyArgLysAlaArgProArgArgAlaIleAl
                                                                                                                                                                                                                                                                                         hrGluGluSerGlnAspValValProPheLeuGluGlnLeuValArgPro
                                                                                                                                                                                                                                                                                                                                         GGAGCTGGTGGCAGAGGAGGACCAGGACCCGTCGGAACTGAATCCCCAGA
                                                                                                                                                                                                                                                                                                                                                           uGluLeuThrAlaGluAspArgArgGluProProGluLeuAsnProGlnT
                                                                                                                                                                                                                                                                                                                                                                                                           CGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGC
                                                                                                                                                                                                                                                                         CAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                             ValSerLeuGlySerTrpAlaThrLeuSerAlaGlnGluProSerGlnGl
                                                                                                                                    1999-205191/17
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4.803
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seq_documentation_block:
ID ABL21473 standard;
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                                                                                                                                                    New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                   Venter
                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                          WO200171042-A2
                                                                                                                                                                                                                                                                                                                                               pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                       Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
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|TOTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGCCCTGCGCTGC
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                                                                                                                                                                                2001-656860/75
                                                                                                                                                                                                   JC,
                                                                                                                                                                                                                                                                                                                                                                            melanogaster
                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide.
cal; gene; ds.
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2000US-0614150
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                                                                                                                                                   detection reagent for detecting for elucidating cell signalling
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                                                                                                                                                    1000
                                                                                                                                                     cell-cell
                                                                                                                                                            or
                                                                                                                                                              more
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capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The invention relates

Claim 1; SEQ ID NO 15892; 21pp + Sequence Listing; English

to an isolated nucleic acid detection

reagent

is

The sequence data for this patent did not form specification, but was obtained in electronic i

m part of the printed format directly from

WIPO

ftp.wipo.int/pub/published_pct_sequences

SQ

Sequence

978

BP;

289

? 261

ű 238

G; 190

T; 0

other;

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- XXX DXXXXX ID
                                                                                                                                                                                   seq_documentation_block:
ID AAV41377 standard;
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                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV41377
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             RANK; necrosis factor-kappa B; NF-kB;
                                                        NF-kB
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                                                                                                  08-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGGTGAATCTCTTTTCA
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                                                                                                                                                                                                                                                                                                                                   AlaAlaProPheLeuThrTyrPheGlyLeuPheGlnVal 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uValHisProArgProGlyGlnAspGlyAlaGlnAlaGlyValAspGlyT 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGA...CAC
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                                                                                                                                                                                                                                                                                                                                                                                  AGAGGATCCATCTGAAGGACATTCACAACGATCGCAATGCAGTTCTGCGG
                                                   receptor activator RANK ligand (RANKL) encoding
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             receptor activator; human;
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alignment_block: US-09-245-198A-2 x AAV41377

Align seg 1/1 to: AAV41377

from: 1

to: 1630

19 rLeuGlySerTrpAlaThrLeuSerAlaGln...GluProSerGlnGluG | :::::: ::: |||||| :::|||:::::: 78 TCCATGTTCCTGGCCCTCCTGGGGCTGGGACTGGGCCAGGTGGTCTGCAG 3 SerLeuGlyLeuAlaLeuAlaCysLeuGlyLeuLeuValValValSe

35 127 19

alignment_scores: Quality: Ratio: Percent Similarity:

106.50 0.772 50.000

Percent

Gaps: Identity:

276 13 24.275

Length:

Sequence 1630 BP;

436 A;

355 C;

379 G; 460 T; 0 other;

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14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                           allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-KB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                       This cDNA encodes a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor kappaB (NF·kB)) polypeptide. RANK is member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF·kB, by contacting a cexpressing membrane-associated RANK with a soluble RANK which bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson DM,
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RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
                                                                                                                                                                                                                                                                    RANK ligand (RANKL). RANKL polypeptides can activate RANK and used to induce maturation of dendritic cells and enhance their
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; Pages 55-57; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-377657/32.
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96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "murine RANKL (ligand for RANK)"
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seq_documentation_block:
ID AAV41371 standard; cf
XX
AC AAV41371;
XX
DT 08-OCT-1998 (first of
XX
DE NF-kB receptor active
XX
                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV41371
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                     NF-kB receptor activator RANK ligand (RANKL) encoding cDNA
                                                                                                                                                  AAV41371 standard; cDNA; 1630 BP
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23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NR-KB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NR-kB by RANK antagonists may be useful in amediorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This cDNA encodes a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding
                                   128
                                                                                                                                                                                                                                                                                                                                                                Sequence 1630 BP; 436 A;
                                                                                                                                                                                                                                                                                                                                                                                                  can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated receptor activator of necrosis factor-kappa B for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis
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                                                                                                                        3 SerLeuGlyLeuAlaLeuAlaCysLeuGlyLeuLeuLeuValValValSe
luLeuThrAlaGluAspArg....
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Murine; receptor activator of nuclear factor kappaB ligand; RANKL; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; timmune response; inflammatory response; graft-versus-bost reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption;
                                                                                                             Murine receptor activator of NF kappaB ligand (RANKL) cDNA
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                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                              CDNA; 1630
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                                                                      NF;
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Sequence 1630 BP;

436 A;

355 C;

379 G;

460 ,

0 other;

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cc kappab (RANK) proteins and their corresponding DNAS. RANK is a member cof the tumour necrosis factor (TNF) receptor superfamily and associates with TNF receptor associated factor (TRAF) 2 and 3 which are important cc with TNF receptor associated factor (TRAF) 2 and 3 which are important cc in the regulation of immune and inflammatory response. The receptors cc are useful for regulating immune response and in screening for inhibitors of signal transduction, e.g. for screening the cmolecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, cc TRAF5 and particularly TRAF6. NF-kappab inhibition by RANK antagonists care useful in ameliorating the negative effects of an inflammatory cresponse that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory creactions and the effects of bone resorption. RANK acts as an anti-cappoticit signal and rescue the cells that express RANK from apoptosis. Cc soluble forms of the receptor are used in vivo or in vitro based cappotionists of RANK-mediated NF-kappa B activation, or to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1996;
07-MAR-1997;
22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that express RANK -
                                                                                                                                               transduction of a signal via RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast precursors and for modulating osteoclast function and activities. They are used as inhibitors of diseases associated with excess bone resorption
                                                   and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Column 63-66; 47pp; English
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07-MAR-1997;
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                                 RANK ligand
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97US-0996139.
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/note= "CD
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                                     (RANKL) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ct= "Murine RANK ligand (RANKL) protein"
"CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor activator of nuclear factor (NF)-
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                                                                                                                tor analysis
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTT 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCATGTTCCTGGCCCTCCTGGGGCTGGGACTGGGCCAGGTGGTCTGCAG
GAAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCGGATCAAGA
                              SerLeuArgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPh
                                                                                                                                         CCTGATGAAAGGAGGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCC
                                                                                                                                                                            sLeuGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCAT.....AAAGTCACTCTGTCCTTGGTACCACGATCGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCTGACTCCTGCAGGAGGATGAAACAAGCCTTTCAGGGGGCCGTGCAGA 318
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                                                                                                                                                                                                                                                LeuAspLeuLeuVal.....AsnGlyValLeuAlaLeuArgCy 167
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                                                                 ACTTTTATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAA
                                                                                                   rgLeu.....CysGlnValSerGlyLeuLeuProLeuArgProGlySer 198
                                                                                                                                                                                                                CTGATGGTGTATGTCGTTAAAACCAGCATCAAAATCCCAAGTTCTCATAA
                                                                                                                                                                                                                                                                                      GCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG
                                                                                                                                                                                                                                                                                                                                                           AAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTT
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Percent Identity:
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1996;
07-MAR-1997;
14-OCT-1997;
                                                                                                                 The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is murine RANKL CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein; s
                                                                                                                                                                                                                                                                                               New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                    Example 7; Column 57-60; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-407216/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD08714 standard; cDNA; 1630
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                                                                                        Sequence 1630 BP; 436 A; 355 C;
                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                           Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine receptor activator of NF-chi B ligand (RANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCGACGTACTTTGGGGCTTTCAAAGTT
                               Quality:
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97US-0077181.
97US-0064671.
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/note= "CDS does not include start codon"
106.50
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                                                                                       379 G; 460 T; 0 other;
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alignment_block: US-09-245-198A-2

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Percent Similarity:

Percent

Gaps: Identity: Length:

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to: AAD08714

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                                                                                                                                                                                                               rgLeu.....CysGlnValSerGlyLeuLeuProLeuArgProGlySer 198
                                                                                                                                                                                                                                                                                                sLeuGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGCCAAGATCTCTAACATGACG.....TTAAGCAACGG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...ThrLysIleAsnSerSerSerProLeuArgTyrAspArgGlnIleGl 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laGlnAlaGlyValAspGlyThrValSerGlyTrpGluGlu..... 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgGluProProGluLeuAsnProGlnThrGluGluSerGlnAspValVa 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....ATATCAGAAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  luLeuThrAlaGluAspArg.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGA....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCATGTTCCTGGCCCTCCTGGGGCCTGGGACTGGGCCAGGTGGTCTGCAG 12
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TGCGACGTACTTTGGGGCTTTCAAAGTT
                                        eLeuThrTyrPheGlyLeuPheGlnVal 224
                                                                                    GAAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCGGATCAAGA 844
                                                                                                                          SerLeuArgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPh 215
                                                                                                                                                                       ACTITIATICCATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAA 794
                                                                                                                                                                                                                                                          CCTGATGAAAGGAGGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCC 744
                                                                                                                                                                                                                                                                                                                                          CTGATGGTGTATGTCGTTAAAAACCAGCATCAAAATCCCAAGTTCTCATAA 694
                                                                                                                                                                                                                                                                                                                                                                                     LeuAspLeuLeuVal......AsnGlyValLeuAlaLeuArgCy 167
                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ysGlnValHisPheAspGluGlyLysAlaVal.....TyrLeuLys 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yGluPheThrValIleArgAlaGlyLeuTyrTyrLeuTyr.....C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gAlaIleAlaAlaHisTyrGluValHisProArgProGlyGlnAspGlyA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....GlyArgLysAlaArgProArgAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..PheLeuGluGlnLeuValArgProArgArg....SerAlaProLys 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTGACTCCTGCAGGAGGATGAAACAAGCCTTTCAGGGGGCCCGTGCAGA 318
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alignment_block: US-09-245-198A-2 x AAD05903

Percent Similarity:

alignment_scores

Quality: Ratio:

106.50 0.772 50.000

Percent

Identity:

Gaps:

13 24.275

Sequence 1630 BP; 436 A; 355 C; 379

G; 460 T; 0 other;

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factors (TRAFS). Triggering of RANK by overexpression or co-expression of factors (TRAFS). Triggering of RANK by overexpression or co-expression of factor RANK and membrane bound RANK ligand (RANKL) results in upregulation of the transcription factor that is most extensively utilised in cells of the immune system.

Inhibition of Nf kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct gene-activating mutations, associated with e.g. familial expansile costeolysis (FEO) and early onset paget's disease of bone (EP). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                       The present invention relates to a novel receptor, referred to as (receptor activator of NF (nuclear factor)-kappaB), a member of To (tumour necrosis factor) receptor superfamily. RANK is a Type I transmembrane protein that interacts with TNF receptor-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine RANKL (receptor activator of NF-kappaB ligand) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD05903 standard; cDNA; 1630 BP
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Page 72-74; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA encoding a receptor activator of NF-kappaB polypeptide treatment of Paget's disease and Familial Expansile Osteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson DM, Hughes
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                                     present sequence
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DB; AAE01992.
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/product= "Murine
NF-kappaB ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 3..887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                   is a cDNA encoding murine RANKL (muRANKL) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANKL (receptor protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activator
                                                                                                                                                                                                                                                                                                                                                               referred to as RANK a member of TNF
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Align seg 1/1 to: AAD05903 from: 1 to: 1630
                                                                  510 TGGGCCAAGATCTCTAACATGACG......TTAAGCAACGG 544
                                                                                                                                                                                              112 ...ThrLysIleAsnSerSerSerProLeuArgTyrAspArgGlnIleGl 127 :::||||||::::: |:
                                                                                                                                                                                                                                                                 419 CCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ..PheLeuGluGlnLeuValArgProArgArg.....SerAlaProLys 73
||||:::::::||| |||:::|||
319 AGGAACTGCAACACATTGTGGGGCCCACAGCGCCTTCTCAGGAGCTCCAGCT 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 ....ATATCAGAAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 CATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGA.... 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 ACCTGACTCCTGCAGGAGGATGAAACAAGCCTTTCAGGGGGGCCGTGCAGA 318
                                                                                                                                                                                                                                                                                                       98 laGlnAlaGlyValAspGlyThrValSerGlyTrpGluGlu...... 111
                                                                                                                                                                                                                                                                                                                                                                                                                  81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SerLeuGlyLeuAlaLeuAlaCysLeuGlyLeuLeuLeuValValValSe 19
ysGlnValHisPheAspGluGlyLysAlaVal......TyrLeuLys 154
                                                                                                        yGluPheThrValIleArgAlaGlyLeuTyrTyrLeuTyr......C 141
                                                                                                                                                                                                                                                                                                                                                                                                          gAlaIleAlaAlaHisTyrGluValHisProArgProGlyGlnAspGlyA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1Pro...... 59
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GAAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCGGATCAAGA 844 SerLeuArgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPh 215 ACTTTTATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAA 794

141

167 sLeuGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuA 184

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Database length: 1873333701
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Database: GenF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query:
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AR140407 Sequence 1 from pater
AF030099 Homo sapiens TWEAK mH
AX201324 Sequence 3 from Pater
AF055872 Homo sapiens Apo3/DR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | BC019047 Homo sapiens, Similar
| AC069459 Mus musculus chrome
| AL603707 Mouse DNA sequence
| AC016876 Homo sapiens clone
                                                                              AY070219 Homo sapiens lymphotox L11016 Homo sapiens lymphotox; AL451008 Homo sapiens chromos; AL350009 Homo sapiens chromos; Y14768 Homo sapiens DNA, cosm
                                       AP000505 Homo sapiens genom Continuation (10 of 11) of
                     AL662801 Homo sapiens chrom
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ThrGluGluSerGlnAspValValProPheLeuGluGlnLeuValArgPr 67
                                       GGTCAGCCTGGGGAGCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGG
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TWEAK, a new secreted ligand in the tumor necrosis factor family that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus TWEAK mRNA, AF030100
                                                                                                                                                                                                                                                                                                                            Submitted (14-OCT-1997) Cell Biology, Biogen, 12 Cambridge Center, Cambridge, MA 02142, USA
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                                                                                                                                                                                           /note="ligand in the TNF family; secreted protein"
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35 ! AP002482 Oryza sativa g
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25 ! AC061972 Homo sapiens c
55 ! AC079384 Homo sapiens 1
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; 1 (bases 1 to 1306) Chicheportiche,Y., Bourdon,P.R., Xu,H., Hsu,Y.M., Sc
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118 375 101 85

325

275 89 225 51 175 35

Hominidae;

Euteleostomi; Homo

linear

20-DEC-1997

218

675 201 625 185

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JOURNAL
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AUTHORS
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US-09-245-198A-2 x AF030099
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                                                     ValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSe 118
                                                                                                       laHisTyrGluValHisProArgProGlyGlnAspGlyAlaGlnAlaGly
                                                                                                                                         luLeuThrAlaGluAspArgArgGluProProGluLeuAsnProGlnThr
                                                                                                                                                                                                                                                                                                                  lSerLeuGlySerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluG
                                                                                                                                                                                                                                                                                                                                                                     LeuSerLeuGlyLeuAlaLeuAlaCysLeuGlyLeuLeuLeuValValVa
GluGluSerGlnAspValValProPheLeuGluGlnLeuValArgProAr
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                                                                                         GTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAG
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Ratio:
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J. Biol. Chem. 272 (51), 32401-32410 (1997)
98070415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-OCT-1997) Cell Biology, Biogen, 12 Cambridge Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hession,C., Garcia,I. and Browning,J.L.
TWEAK, a new secreted ligand in the tumor necrosis factor family
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4.744
95.982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ligand in the TNF family; secreted
codon not verified experimentally"
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/db_xref="taxon:9606"
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/map="17p13"
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18. .767
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Gaps: 0
Identity: 88.839
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seq_name: gb_pat:AX201324
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                                                                                                                   luLeuThrAlaGluAspArgArgGluProProGluLeuAsnProGlnThr
                                                                     lSerLeuGlySerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1353)
1 (bases 1 to 60ddard,A., Godowski,P.J., Gurney,A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1353 bp
Sequence 3 from Patent WO0153486.
AX201324
                                                                                                                                                                                                                                                                                                       Quality:
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JOURNAL
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SOURCE
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ACCESSION
                                                                                                                                                                                                                                                                              seq_name: gb_pr:AF055872
                                                                                                                                                                                                                                                  q_documentation_block:
CUS AF055872
                                JOURNAL
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                    Submitted (25-MAR-1998) Molecular Oncology, South San Francisco, CA 94080, USA
                                                                                                          apo3
                                                                                                                                  Marsters, S.A., Sheridan, J.P., Pitti, R.M.,
                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                          Direct
                                                     Ashkenazi, A.
                                                             Marsters, S.A., Sheridan, J.P.,
                                                                                    98228355
                                                                                                                                                                                  Homo sapiens
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                                                                                                                   Identification of a ligand
                                                                                                                                                  (bases 1 to 1368)
                                                                        (bases 1 to 1368)
                                                                                             Biol. 8 (9),
                                          Submission
Location/Qualifiers
1. 1368
                                                                                             525-528
                                                                                             (1998)
                                                                                                                  for the death-domain-containing
                                                                                                                                                                                                                                     bp mRNA
(APO3L) mRNA,
                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                              Pitti, R.M.,
                                                             Brush, J.,
                                                                                                                                       Brush,J.,
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alignment_block:
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|CAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAG
rProLeuArgTyrAspArgGlnIleGlyGluPheThrValIleArgAlaG
                                                                                                                                                                                                                                     ValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSe
                                                                                                                                                                                                                                                                                                        laHisTyrGluValHisProArgProGlyGlnAspGlyAlaGlnAlaGly
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                                                                                        CCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTG
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                                                                        GGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTC
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Ratio: 4.744
nilarity: 95.982
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XYLYCQVHFDBGKAVYLKLDLLWDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL
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443 c 389 g 264 t
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58. .807
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1. .1368
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alignment_scores:
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US-09-245-198A-2 x AX180714
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                                                   uLeuThrAlaGluAspArgArgGluProProGluLeuAsnProGlnThrG
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Sequence 1 from Patent WO0145730.
AX180714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                artificial sequence.
1 (bases 1 to 898)
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RINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGYLALRCLEE
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266 c 267 g 178 t
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52. .873
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                                                                                                                                                                                                                                                                  Homo sapiens, superfamily, me complete cds. BC019047
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                 Gaithersburg, Maryland;
                                                                                                                                                                            Strausberg, R.
                                                                                                                                                                                                                        Homo sapiens
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        Web site:
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102 alaspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSer 118
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Submitted (07-DEC-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Geno
                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Con DNA Sequencing by: National Institutes of I Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1651 bp mRNA, Similar to tumor necrosis member 12, clone MGC:20669
http://www.nisc.nih.gov/
nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                Consortium (LLNL)
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IMAGE: 4766071,
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GGAGGTTACACAACTTGTCTGAGGCCATGAGATACTAAGTGGTGGAGCCA 530
                                                                                                                                                                                 CAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lSerLeuGlySerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluG 35
                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 30 Row: p Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507596. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Brooks,S., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
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4.418
70.395
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superfamily, member 12"
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ARRAIAAHYEVHPRPGQDGAQADGGYTTCLRP"

1 517 c 481 g 309 t
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/tissue_type="Primary B-Cells from
/clone_1ib="NIH_MGC_48"
/lab_host="DH10B-R"
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/db_xref="taxon:9606"
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531 AGATTTGAACCCAGCTAGAATGTGCCTGTGTACTGGACATGGTCTGCATG 580	HORSE PARIS	AAAGGCGAAGGTGGCTGGTGCAGGGGTGAAGGGGCCAAAAGGAAGG
	00 .	
00	81 A	AAGGCGAGGTGGCTGGTGCAGGGGTGAGGGGTCCATGCAGGGGCCACAT 63
00	00 .	
0081 AAAGGCGAGGTGGCTGCAGGGGTGCAGGGGTCCATGCAGGGGCCACAT	31	CAAAAAGGGGAGAGGGAAGTTTCCAGAAAGAAGAGAGAGA
0081 AAAGGCCGAGGTGGCTGGTGCAGGGGTGAGGGGTCCATGCAGGGGCCACAT 00	01 ·	GlyValAspGlyTh 10
00	05 r	ValSerGlyTrpGluGluThrLysIleAsnSerSerSerProLeuArgT 12
00	22 1	TASPATGGlnIleGlyGluPheThrVallleArgAlaGlyLeuTyrTyr 13 :::
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81 AAAGGCGAGGTGGCTGGTGCAGGGGTGAGGGGTCCATGCAGGGGCCACAT 81 AAAGGCCAGGGTGGCGTGGTGCAGGGGTCCATGCAGGGGCCACAT 81 ACAGGCGAGGGTGGCGGAGAGTTTCCAGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	55 81	nGlyValLeuAlaLeuArgCysLeuGluGluPheS 17 :
81 AAAGGCGAAGGTGGCTGGTGCAAGGGGTGCAATGCAAGGGGCCACAT 81 AAAGGCGAAGGTGGCTGGTGCAAGGGGTGCAATGCAAGGGGGCCACAT 81 AAAGGCGAAGGTGGCTGGTGCAAGGAAGAAGAAGAAGAAGAAGAACAATCTCCC 90	2 6	rAlaThrAlaAlaSerSerProGlyProGlnLeuArgLeuCysGlnVal 18
AAAGGCGAGGTGGCTGGTGCAGGGGTGAGGGGTCCATGCAGGGGCCACAT AAAGGCGAGGTGGCTGGTGCAGGGGTGAGGGGTCCATGCAGGGGCCACAT CCCAAAAAGGGGAGAGGAAGTTTCCAGAAAGAAGAAGAAGACACATCTCCC CCCAAAAAGGGGAAGAGGAGAAGAAGAAGAAGAAGAACACATCTCCC CCCAAAAAAGGGGAAGGGTCAAAGGAACAAGAAGAAGAAGACACACATCTCCCC CCCAAAAAAGGGGAAGGGTCAAAGGAACAAGAAGAAGACAGGTGTGGAAGGACCACGTGTGGAAGGACCAAGGTGTGGAACAGGTCTGAACAGGTCTGAACAGCTCTAGCACTTTAAAACAACAACAAGCTCCAGCCCTCTGCGCT IIIIIIIIIIIIIIIIIIIIIIIIII	89 S	erGlyLeuLeuProLeuArgProGlySerSerLeuArgIleArgThrLe 205 CTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGGATCCGCACCCT 103
AAAGGCGAAGGTGGCTGGTGCAAGGGGTGAAGGGGTCCATGCAAGGGGCCACAT 630 CCCAAAAAGGGGAAGGGAAAGTTTCCAGAAAAGAAAGAAGAAGAAGAAGAAGAAAAGGGAAAGGAAGGGAAAGTTTCCAGAAAAAAAA	205 u	ProTrpAlaHisLeuLysAlaAlaProPheLeuThrTyrPheGlyLeuP 222
581 AAAGGCGAGGTGGCTGGTGCAGGGGTGAGGGGTCCATGCAGGGGCCACAT 630 581 AAAGGCGAGGTGGCTGGTGCAGGGGTGAGGGGTCCATGCAGGGGCCACAT 630 100	222 h 081 T	eGlnValHis 225 CAGGTTCAC 1091
581 AAAGGCGAAGGTGGCTGGTGCAAGGGTGAAGGGTCCATGCAAGGGCCACAT 630 100	q_name: q_docume CUS FINITION	gb_htg:AC069459 entation_block:
100	SION ON RDS E	AC069459 AC069459 AC069459:23 GI:14547768 HTG; HTGS_PHASEL; HTGS_DRAFT; HTGS_FULLTOP. house mouse. M Mus musculus
100	EFERENCE AUTHORS	eleostomi rinae; Mu rinae; Mu rinae; Mu rinae; Mu rinae; Mu rinae; Mu rinae; Mu rinae; Mu rinae; Mu rinae; Mu
100		gues,M., , Kelly, rtin,R., rris,S.,

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BASE COUNT
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alignment_block:
US-09-245-198A-2 x AC069459/rev
                                                                                                                                         alignment_scores
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                                                                     Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baylor Plaza,
On Jun 25, 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S., Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length
(see http://www.hysc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
                                                                                             Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer Bodipy: 48% of reads
Chemistry: Dye-terminator Big Dye: 52% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 212648 bases at least Q40
Consensus quality: 218902 bases at least Q30
Consensus quality: 222384 bases at least Q30
Estimated insert size: 210656; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
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62253
118773
118873
148925
149025
167232
167332
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169008
190008
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Center clone name: RP23-188P5
----- Summary Statistics
Sequencing vector: M13; L08821
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------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
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                                                                   602.50
4.782
70.000
                                                                                                                                                                                                                                                          /clone="RP23-168P5"
                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149024: gap of unknown length
167231: contig of 18207 bp in length
167331: gap of unknown length
189907: contig of 22576 bp in length
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196537: contig of 6530
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                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_ro:AL603707
Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 20, 2001 this sequence version replaced gi:16605765. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wit only a small overlap as described above.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 234182)
                                                                                                                                                                                                                                                                                                                                                                             complete sequence. AL603707
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                                                                                                                                                                                                                      Pearce, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 rSerSerProLeuArgTyrAspArgGlnIleGlyGluPheThrValIleA 133 ·
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                           euAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerPro 179
                                                                                                                                                                                                                                       AGGCAGAGGTCTGGATTTGCTTGCCTCTCTCTGTTCCAGGTGCACTTTGA 66310
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                                                                                                                     TGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAACGGTGTGC
                                                                                                                                                                         pGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAsnGlyValL 163
                                                                                                                                                                                                                                                                                        Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-422L16 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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complement(84,050. .84131)
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/note="Sequence from uni-directional primer reads
big dye terminator reads only."
s 56824 c 57519 g 60529 t
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/chromosome="11"
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REFERENCE
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LOCUS AC016876
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TITLE
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B lirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

B aliwrin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferrelra, P., Fitthugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Weldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W.J., Zimmer, A., and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 3, 2001 this sequence version replaced gi:13431059. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapieus chromosome, clone RP11-186B7
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Insert size: 168000; agarose-fp
Insert size: 188858; sum-of-contigs
Quality coverage: 8.1 in Q20 bases; agarose-fp
Quality coverage: 7.2 in Q20 bas.
NOTE: This is a 'working draft' sequence. It curr
consists of 16 contigs. The true order of the pie
                                                                                                                                                                                          Sequencing vector: M13; M77815; 3% of reads Sequencing vector: Plasmid; n/a; 97% of reads Sequencing vector: Plasmid; n/a; 97% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960/31 Consensus quality: 181928 bases at least Q40 Consensus quality: 185529 bases at least Q30 Consensus quality: 187335 bases at least Q20 Consensus quality: 187335 bases at least Q20 Consensus quality: 187335 bases at least Q20 Consensus quality: 187335 bases at least Q20
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draft' sequence. It currently The true order of the pieces
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FEATURES
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20704 20803: gap of 100 bp
20804 21935: contig of 1132 bp in length
21936 22035: gap of 100 bp
22036 22020: contig of 2167 bp in length
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94726. .102564
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68265. .94625
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22036. .24202
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/clone_lib="RPCI-11 Human Male
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/db_xref="taxon:9606"
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seq_name: gb_htg:AC098923
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US-09-245-198A-2 x AC016876/rev
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                                            TyrPheGlyLeuPheGlnValHis
                                                                                                                                                                                                                                                                                  alTyrLeuLysLeuAspLeuLeuValAsnGlyValLeuAlaLeuArgCys 167
                                                                                                                                                                                                                                                                                                                             ACTCGGCCTGTTGTCCCCACCCCAGGTGCACTTTGATGAGGGGGAAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACTTCGGACTCTTCCAGGTTCAC
                                                                                       GGATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCCTTCCTCACC
                                                                                                       rgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPheLeuThr 217
                                                                                                                                                  CCTCTGCCAGGTGTCTGGTCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGC
                                                                                                                                                             gLeuCysGlnValSerGlyLeuLeuProLeuArgProGlySerSerLeuA
                                                                                                                                                                                                                       LeuGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuAr
                                                                                                                                                                                                                                                                    TCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGCCCTGCGCTGC
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/note="assembly_fragment
clone_end:T7
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seq_documentation_block:
LOCUS AC098923

AC098923 179030 bp DN Rattus norvegicus clone CH230-154B15,

DNA

linear HTG 20-DEC-2001 SEQUENCING IN PROGRESS

DEFINITION

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JOURNAL
REFERENCE
AUTHORS
TITLE
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of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064677.
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AC098923.4 GI:17973852
HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                           Center project name: GIOK
Center clone name: CH230-154B15
Center clone Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College o
Consensus quality: 137096 bases at least Q40 Consensus quality: 145080 bases at least Q30 Consensus quality: 152950 bases at least Q20 Estimated insert size: 138980; sum-of-contiqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.990329First
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Rodentia;
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Sciurognathi; Muridae;
      sum-of-contigs estimation
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Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 68 contigs. The true order of the pieces is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved 94952 95052 98587 98687 100598 102698 102797 102867 105238 107406 107406 109058 1119555 111555 68499
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alignment_scores:
    Quality:
    Ratio:
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US-09-245-198A-2 x AC098923/rev
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134 laGlyLeuTyrTyrLeuTyrCys..
                                                                                                                                         101 GlyValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSe 117
                                                                      rSerProLeuArgTyrAspArgGlnIleGlyGluPheThrValIleArgA 134
                                                      CAGCCCTCTGCGCTATGACCGCCAGATTGGGGGAATTTACGGTCATCAGGG
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus mRNA for putative CD154 (CD40 ligand).
                                                                                                                                                                                                                                                                       2 (bases 1 to 892)
Tregaskes,C.A.
Direct Submission
Submitted (24-JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ243435.1 GI:8977828 CD154 gene.
                                                                                                                                                                                                                                                                                                                                   cloning of a putative Unpublished
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Tregaskes, C.A., You
                                                                                                                                                                                                                                                            Animal Health, High
              /codon_start=1
/product="putative CD154
/protein_id="CAB95748.1"
/db_xref="GI:8977829"
                                                                                         /gene="CD154"
73. .891
                                                                                                                       /tissue_type="spleen"
73. .891
                                                                                                                                                    /strain="white leghorn Line
/db_xref="taxon:9031"
/clone="chcd4012.2"
                                                                         /gene="CD154"
                                                                                                                                                                                                 /organism="Gallus gallus"
translation="MNEAYSPAAPRPMGSTSPSTMKMFMCFLSVFMVVQTIGTVLFCL"
                                                                                                                                                                                                                               Location/Qualifiers
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tative chicken CD40 ligand
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  CCAGTCCATCCGGGAGGGCGGTGTCTTCGAGCTGCGGCAGGGCGACATGG
                                        1.....SerGlyLeuLeuProLeuArgProGlySerSerL 200
                                                                                                                        SerAlaThrAlaAlaSerSerProGlyProGlnLeuArgLeuCysGlnVa 188
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SEELPKEMHRSHEHPHLKSRNETSVAEEKKQPLATHLAGVKSWTTVRVLKMMTTSYA
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LDTHSTSTALCELQSIREGGVFFLRQGDMVFVNVTDSTAVNVNDGNTYFGMFKL*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP11-168F24 is from the library RPCI-11.1 constructed at the
Roswell Park Cancer Institute by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone RP11-168F24 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-306F2 is at 108868 in this sequence right end of clone RP3-401012 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          feature key.

The following abbreviations are used to associate primary accession members given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL353138 108967 bp DNA linear PRI 16-OCT-2000 Human DNA sequence from clone RP11-168F24 on chromosome 6, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requests: clonerequest@sanger.ac.uk
On Oct 17, 2000 this sequence version replaced gi:10799557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peck, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                          1061. .1121
                                                                                                                                                                           complement(1.
                                                                                                                                                                           /clone_lib="RPCI-11.1"
complement(1. .355)
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .108967
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                     /clone="RP11-168F24"
                                                                                                                                                                                                                                                                       /chromosome="6"
                              /note="MIR repeat: matches
                                                                                                                                                   note="match: GSS:
                                                                                     'note="MER5B repeat: matches 29.
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Primates;
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                                                                                                                                               Em: AQ230925
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                              70.
                                 . 129
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                              of consensus"
                                                                                        of consensus"
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                                                                                                                                                                                                                                                                                                                                                  /note="31 copies 2 mer gg 72% conserved" complement(15328. .15962) /note="match: GSS: Em:AQ631047"
                                        /note="L1MC4 repeat: matches 6487. .6609 of consensus" 21659. .22737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9572. .9811

/note="MIR repeat: matches 3. .247

complement(10614. .11080)

/note="match: GSS: Em:AQ571033"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ760102"
9190. .9605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER53 repeat: matches 1..186 of consensus"
3255..3292
/note="19 copies 2 mer tt 92% conserved"
3878..3954
/note="L2 repeat: matches 2164..2237 of consensus 4113..4282
                                                                                                                                                                                  complement(16128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluJb repeat: matches 2.
complement(6576. .7026)
   /note="TIGGER1 repeat: matches 1324. .2412 of consensus"
22738. .23149
                                                                                          note="LIMC3 repeat: matches 6631.
                                                                                                               /note="21 copies 2 mer gt 97% conserved"
17613. .18726
                                                                                                                                                                   note="match: STS:
                                                                                                                                                                                                         /note="match:
                                                                                                                                                                                                                         /note="match: GSS: Em:AQ418183"
15991. .16438
                                                                                                                                                                                                                                                                             note="14 copies 2 mer tg 89% conserved"
                                                                                                                                                                                                                                                                                                                 note="match: GSS: Em:AQ126356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="25 copies 2 mer tt 80% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2636. .2749 of
l3889. .13938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )190. .9605
/note="match: GSS: Em:B90415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9989. 9080
/note="MIR repeat: matches 51. .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:B32322"
1640. .7672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3442. .5744
/note="AluSc repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER5A repeat: matches 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"MIR repeat: matches 201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MER5A repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MER5B repeat: matches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="MER5A repeat: matches 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="MER5A repeat: matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                te="Alu repeat: matches 253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :..7771
:e-"MER5A repeat: matches 4. .112 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6856
                                                                                                                                                                                                                                                               .16456
                                                                                                                                                                                                                                                                                                                                                                                                            by copies 2 mer cc 62% conserved".15285
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                                                                                                                                                                                  GSS: Em:AQ815493"
128. .16449)
                                                                                                                                                                 Em: HS015XG5"
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                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37351...37408 .--- marches 1...303 of /note="29 copies 2 mer aa 72% conserved" 37423...37571
                                  109.50
1.117
44.344
                                                                                                                           41485. 41800
/note="Alux repeat: matches 1. .310 of consensus"
41802. .41839
                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ778077"
39069. .39496
                                                                                                                                                                                                                                                                                                                                                /note="26 copies 2 mer ac 92% conserved" complement(38539. .39048)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER5A repeat: matches 2. .188 of consensus" 37565. .37656 /note="MER5A repeat: matches 1. .105 of consensus" 37723. .38025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31187. .32501
/note="Cheshire repeat: matches 1. .1360 of consensus"
33567. .33766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30805. .31116
/note="AluSx repeat: matches 11. .312 of consensus"
31117. .31175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29268. .29531

'note="Cheshire repeat: matches 2216.

29499. .29926

'note="match: GSS: Em:AQ617879"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27895. 28024 .... marches 2. .204 of consensus" /note="MIR repeat: matches 111. .246 of consensus" 29211 ... 29252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26054. .26081
/note="14 copies 2 mer tt 100%
27311. .27518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24920. .25222
/note="AluY repeat: matches 1. .303 of consensus"
25712. .25869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER57A repeat: matches 1 .434 of consensus"
23150 .23658
/note="TIGGER1 repeat: matches 774 .1326 of consensus"
                                                                                                                                                                                                                                          /note="match:
39334. .39389
                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ570301"
39057. .39524
                                                                                                                                                                                                                                                                                                                                                                                          38062.
                                                                                                                                                                                                                                                                                                                                                                                                                       complement(37990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MLT1E repeat: matches 255. .560 of consensus"
30142. .30804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29820. .30127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23655.
                                                                                                                                                                                                      /note="MIR repeat: matches 90. .145 of consensus"
40906. .41237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23655. .24186
/note="TIGGER1 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSx repeat: matches 8.
complement(37990. .38488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 48. .261 of consensus"
34845. .35149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ614744"
27427. .27633
                                                                                                                                                                                  note="L1ME1 repeat: matches 5817. .6122 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                          note="match: STS: Em:L18341"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Cheshire repeat: matches 1469. .1528 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Cheshire repeat: matches 1528. .2173 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MLTID repeat: matches 1. .154 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="21 copies 2 mer at 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="MER97c repeat: matches 16.
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                                Length: 221
Gaps: 12
Percent Identity: 24.887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTCCAATAAGACAACAGCCAGGGTGCAAGTGAGGTATCCCAACACTAAA 14145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....CAGCCACAGCCTGGCCAAGATCGAGCGCAGCCTGGCCAGCAGCC 14468
           3-isopropylmalate dehydratase large subunit; 3-isopropylmalate dehydratase small subunit; 3-isopropylmalate dehydrogenase; branched-chain amino acid aminotransferase; carboxyl transferase; delta-1-pyrroline-5-carboxylate dehydrogenase; gltx; glutamyl-tRNA synthetase; histone-like DNA binding protein; hydrolase; ilvE;
synthetase;
leuB; leuC;
                                                                                                                                                                        Streptomyces coelicolor
                                                                                                                                AL031124.1 GI:3355667
                                                                                                                                                      AL031124
                                                                                                                                                                                              SC1C2
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ORGANISM
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97000351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC.
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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Kinashi,H. and Hopwood,D.A.

A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma subunits; ureC.
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-JUL-1998) Streptomyces coelicolor sequencing Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overlapping sections once, or longer, because we arrange small overlap between neighbouring submissions. Cosmid 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequenced clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are also included but some of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redenbach, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkhill,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy,L. and Harris,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Streptomycineae; Streptomycetaceae; 1 (bases 1 to 42210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transfer-RNA-Glu; ureAB; urease alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in codons is given for each CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 42210)
lenbach, M., Kieser, H.M., Denapaite, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 42210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8D9 and 7Al on the AseI-B genomic restriction fragment
                                                                                       /note-"SC1C2.01, probable delta-1-pyrroline-5-carboxylate dehydrogenase, partial CDS, len >408 aa; similar to many e.g. TR:O50443 (BMBL:ALD10186) delta-1-pyrroline-5-carboxylate dehydrogenase (M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 significant matches with motifs in the PROSITE database
                             tuberculosis) (543 aa), fasta scores; opt: 1753 z-score: 2214.2 E(): 0, 65.1% identity in 407 aa overlap, and
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Streptomyces
/strain="A3(2)"
PUT2_HUMAN delta-1-pyrroline-5-carboxylate dehydrogenase
                                                                                                                                                                                                                        /gene="SC1C2.01"
                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:100226"
/clone="cosmid 1C2"
                                                                                                                                                                                                                                                                                      /gene="SC1C2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .42210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit; urease beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fortuitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ge for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The length
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stem_loop
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                                                                                                                                                                                                                                                                                                                                                                                           /gene="leuB"
1744. 2787
/gene="leuB"
1744. 2787
/gene="leuB"
/gene="leuB"
/gene="leuB"
/gene="scitc2.03, leuB, probable 3-isopropylmalate
/note="SC1C2.03, leuB, probable 3-isopropylmalate
dehydrogenase, len: 347 aa; similar to e.g. LEU3_CORGL
3-isopropylmalate dehydrogenase (EC 1.1.1.85) (340 aa),
fasta scores; opt: 1450 z-score: 1318.1 E(): 0, 68.0%
identity in 338 aa overlap. Contains PS00470 Isocitrate
identity in 338 aa overlap. Contains PS00470 Isocitrate
                           /db_xref="Sptrembl:086504"
/translation="MSRSLNLAVIPGDGIGQEVVAEGLKVLSAVLPQDVKLETKEFDF/
/translation="MSRSLNLAVIPGDGIGQEVVAEGLKVLSAVLPQDVKLETKEFDF/
GARRYHATGEFLTDADLALKAHDATLLGAIGDPSVPSGVLERGFLKKLRFAFDHHVN
LRPSKLLPGVATPLAGQPEIDFVVVREGTEGPYTGNGGTIRKGTEHEVATEVSVNTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SC1
1537. .166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hairpin_loop
1522. .1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (563 aa), fasta scores; opt: 1273 z-score: 1730.4 E(): 0, 48.5% identity in 408 aa overlap. Contains PS00687 and PS00070 Aldehyde dehydrogenases glutamic acid active site and cysteine active site and Pfam match to entry PF00171 aldedh, Aldehyde dehydrogenases, score 114.70, E-value
                                                                                                                                             /transl_table=11
/product="3-isopropylmalate
/protein_id="CAA19970.1"
/db_xref="GI:3355670"
                                                                                                                                                                                                                                                                                                                                                         match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MAETTVRRRVRHLSRTSDSDRKNAAAALQRSLDRRDNGGATGH"
1744. . . 2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVYAITPFNFSAIAANLPTAPALMGNVVVWKPSPTQTHAAVLLMQLLEEAGLPKGVIN
LVTGDGIAVSEVALEHRDLAGIHFTGSTKTFQHLWKTVGNNIEKYRTYPRLVGETGGK
DFLVAHPSADRAVLKTALTRGAFEYQGQKCSATSRAYIPASIWNDGFKEEFAAEVDYL
GVERVVRDAFARAQARPRKKLTLVHKNNVLTFAGHLWTN1FNKVAAEYPEVTTDYLHV
                                                                                                                                                                                                                                                                                                                                                      and isopropylmalate dehydrogenases signature and Pfam match to entry PF00180 isodh, Isocitrate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenases, score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECTDPENEVFRTEYFGPFLAVHVYDDSADDAYDAMLTQMESVSDYALTGSVISNDRAA
AAYTMEKLRYAAGNFYINDKSTGAVVGQQPFGGGRASGTNDKAGAPQNLMRWTLTRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:086502"
/translation="IDSPCELIDFWRFNVHYARNILAEQPPANSQGVWNRMDHRPLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="delta-1-pyrroline-5-carboxylate
/protein_id="CAA19968.1"
/db_xref="GI:3355668"
                                                                                                                                                                                                                                                                                                                          isopropylmalate dehydrogenases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:3355669"
/db_xref="SPTREMBL:086503"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein
/protein_id="CAA19969.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SC1C2.02"
/note="SC1C2.02, questionable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfam match to entry PF00171 aldedh, Aldehyde
dehydrogenases, score 114.70, E-value 1.8e-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KETLVAPTDYTYPHMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMGDVTDLSNFIGAVIDERSFAKNKAAIDRAKEDETCTIVAGGSYDDSVGYFVRPTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=2
/transl_table=11
                                                                                                                                                                                                                                                                      /codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="possible RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00070 Aldehyde dehydrogenases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SC1C2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="true overlap with cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1189
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                                                                                                                                                                                                                                                                   _start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SC1C2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LC2.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aldehyde dehydrogenases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with 18bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             upstream of SCIC2.02*
                                                                                                                                                                                                        dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8D9"
                                                                                                                                                                                                                                                                                                                          score 356.60, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cysteine active
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CDS gene RBS

CDS gene

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                             9351
                                                                                                                                                                                                                                                                                                         9451
                                                                                                                                                                                                                           9401 GTTCGTCCTTGGAGCCGAAGTAATACAAGAGGTGGCCGCTGCTCATGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                     66
                                                                                                                                                                                   50
                                                                                                                                                                                                                                                                 35
                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                     GCGCTCGGCGCCGAGGCGCCCTCCCTCCACTCCAGGGTGCGCAGCAGCA
                                                                                                                                                                                 GlnThrGluGluSerGlnAspValValProPheLeuGluGlnLeu.ValA
                                                                                                                                                                                                                                                                                                                                             SerLeuGlySerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluGl
.....IleAlaAlaHisTyrGluValHisProArgProGlyGlnAspGl
                                                           ACCTCGCGGCCGAGCGCCCATGGTGAGCTTC.....TCCAGCCC
                                                                                                   rgProArgArgSerAlaProLysGlyArgLysAlaArgProArgArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                     ç
                                                                                                                                                                                                                                                LeuThrAlaGluAspArgArgGluPro.ProGluLeuAsnPro 49
                                                                                                                                                                                                                                                                                                                                                                                     reverse of:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRGWHDGQLVPYAPLSLDPATMVLHYAQEIFEGLKAYRRPDGSVATFRPEKNGARFQA
SSRRLGMPELPVDTFIEACDALVAQDEKWVPAHGGEESLYLRPFMIATEVGLGVRPAN
EYLFIVIASPAGAYFPGGVKPYSIWVSEDRVRAVPGGMGDAKTGGNYAASLLAQAEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILVE_BACSU putative branched-chain amino acid aminotransferase (362 aa), fasta scores; opt: 1047 z-score: 1401.5 E(): 0, 44.7% identity in 360 aa overlap. Contains PS00770 Aminotransferases class-IV signature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108.50
0.882
54.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4214.
/gene="SC1C2.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4214. .5644)
/gene="SC1C2.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3763. .3852
/gene="ilvE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SC1C2.04, ilvE, probable branched-chain amino acid aminotransferase, len: 362 aa. similar to many, e.g.
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1759. .2766
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VTQRLRDALLDIQRGTVADPHGWMHTLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {	t AKGCDQVCYLDAIERKWVEELGGMNLYFVYGNKIVTPSLTGSILEGVTRDSLLTVARD}
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1.3e-105"
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VHGSAPDI AGQGKADPTATVLSVALLLRHLGYEDEAAR I EDAVSADLGERGDL PARST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PS00770 Aminotransferases
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Percent Identity: 29.333
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  Direct Submission
Submitted (16-MAY-2000) Department of Medicine and University of Washington Genome Center, University Box 352145, Seattle, WA 98195, USA
                                                                                                        Stover C.K., Pham,X. Q.T., Erwin,A.L., Mizoguchi,S.D., War Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spen Wong,G.K.-S., Wu,Z., Paulsen,IT., Reizer,J., Saier,M.H., Hancock,R.E.W., Lory,S. and Olson,M.V.
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147. .584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="PA1763"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                       5309
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complement(7885.
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TLFAASLAHILMRIPELVYFIFTFPAVLLILVAFMLAMGRYRGYRLTELFRFKALLKD
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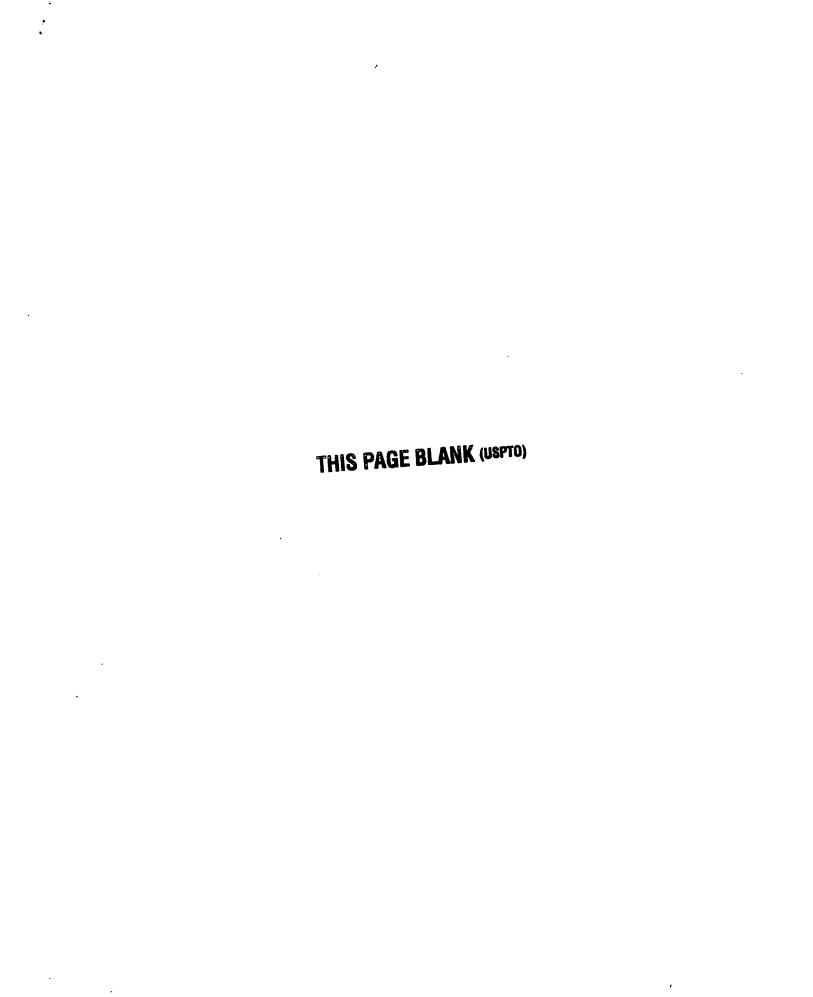
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........CGGCCTGCTGTCCGAGCCGGGTTA 12274
                                 IleGlyGluPheThrValIleArgAlaGlyLeu 136
                                                                                                                                                                                                                                                                                                                laArgProArgArgAla.....
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                                                                                                                                                                                                                                                                                                                                                                         eLeuGluGlnLeuValArgProArgArgSerAlaProLysGlyArgLysA 77
                                                                                                                                                                                                                                                                                                                                                                                                                           CCGCCGCCAGCACCACCGACGGAGGGAGTGGCCAATCCAGTGCGCCGGC 12548
                                                                                                                                                                                                                                                                                                                                                                                                                                           ProProGluLeuAsnProGlnThrGluGluSerGlnAspValValProPh 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..GluProSerGlnGluGluLeuThrAlaGluAsp.....ArgArgGlu 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLeuAlaLeuAlaCysLeuGlyLeuLeuLeuValValValSerLeuGl 21
                                                                     GGAAAAACTCCCGTGCAGGAGGATCACAGGCGGTCCGCCGCCGCTCGCCGG
                                                                                                    rpGluGluThrLysIleAsnSerSerSerProLeuArgTyrAspArgGln 125
                                                                                                                                         AGGTAAGGACCTAATCCGAGCGCACGCGGCGAGTACCAGAAGCGGCGGTT
                                                                                                                                                                       oGlyGlnAspGlyAlaGlnAlaGlyValAspGlyThrValSer...GlyT 109
                                                                                                                                                                                                             CGCGTAGTCGGCGACCCGGTTGTCCCGGTAACCATCGTTGCGAATCGACA 12448
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Result
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Maximum Match 100%
Listing first 45 summaries
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                 Score.
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1 ggtgctgagcctgggcctgg.....ataaatcatgatttctcttc 1168
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7412.656 Million cell updates/sec
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1168)

1 (chicheportiche,Y., Bourdon,P.R., Xu,H., Hsu,Y.M., Scott,H.,

Hession,C., Garcia,I. and Browning,J.L.

TWEBK, a new secreted ligand in the tumor necrosis factor family that weakly induces apoptosis

J. Biol. Chem. 272 (51), 32401-32410 (1997)
Chicheportiche,Y., Bixler,S., Tizard,R. and Browning,J. Direct Submission Submitted (14-OCT-1997) Cell Biology, Biogen, 12 Cambridge Center, Cambridge, MA 02142, USA
                                                                                                                                                                                                                                        Mus musculus TWEAK mRNA, AF030100
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AF030099 Homo sapi
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AC0103598 Homo sapi
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Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
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Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
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Wuzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Direct, Submission
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                                                                         Submitted (31-MAY-2000) Human Genome Seq
of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
On Jun 25, 2001 this sequence version re
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                                                                                                                                                       Worley, K.C.
Direct Submission
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AC069459.23 GI:14547768
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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1 (bases 1 to 203083)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                              Unpublished
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                                                                         Jun 25, 2001 this sequence version replaced g1:12621364
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                   Center code: BCM
                                     Center: Baylor College
site: http://www.hgsc
                                                         Genome Center
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                                       of
 .bcm.tmc.edu/
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                                                                                                               Sequencing Center, Depa
lor College of Medicine,
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NOTE: This is a "vorking draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-primer Bodipy: 48% of reads (hemistry: Dye-terminator Big Dye: 52% of reads Assembly program: Phrap; version 0.990329 (Consensus quality: 212648 bases at least Q40 (Consensus quality: 218902 bases at least Q20 (Consensus quality: 218902 bases at least Q20 (Consensus quality: 218902 bases at least Q20 (Consensus quality: 212384 bases at least Q20 (Consensus quality: 210856; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 7.2x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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62252: gap of unknown length
118772: contig of 56520 bp in 16
118872: gap of unknown length
148924: contig of 30052 bp in 16
149024: gap of unknown length
167231: contig of 18207 bp in 16
167231: gap of unknown length
18907: contig of 22776 bp in 16
190007: gap of unknown length
196337: contig of 6530 bp in length
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                                                                                                                                                                  corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone revenuests: clonerequest@sanger.ac.uk Clonerequests: clonerequest@sanger.ac.uk Clonerequests: clonerequest@sanger.ac.uk Clonerequests: clonerequest@sanger.ac.uk Clonereques
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-422L16 from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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    tgtgcaccaggcactgagatgggctggacctggtggcaggaagccagagaacctgggact
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/chromosome="11"
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/clone="RPG3-422L16"
/clone=11b="RPGI-23"
/clone=164050. 84131)
/note="Sequence from uni-directional primer reads
big dye terminator reads only."
a 56824 c 57519 g 60529 t
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Ashkenazi,A.J., Goddard,A., Godowski,P.J., Hillan,K.J., Marsters,S.A., Pan,J., Pitti,F Stone,D.M., Watanabe,C.K. and Wood,W.I. Compositions and methods for the treatment Patent: WO 0153486-A 3 26-JUL-2001; Genentech, Inc. (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/db_xref="taxon:9606"
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Patent WO0153486.
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Pred. No. 4.7e-154;
0; Mismatches 219;
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AF055872.1 G
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                                                                  Direct
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                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 1368)
                                                   Submitted (25-MAR-1998)
South San Francisco, CA
                                                                          Ashkenazi,A.
                                                                               Marsters, S.A.,
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17p13"
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(APO3L) mRNA,
                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                 Pitti,R.M.,
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                                                                                 Goddard, A.
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                                                                      ctctttcaagttcactgaggggccttgctctcccagattccttaaactttccctggctcc
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33; Conservative
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Apo3/DR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Apo3/DR3 ligand"
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YYLYCOVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLIAL
REGSSLRITTLWWAHLKAAPFLTYFGGLFQVH"
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0; Mismatches 219;
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MEDLINE
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1306) Chicheportiche, Y., Bourdon, P.R., Xu, H., Hsu, Y.M., S Hession, C., Garcia, I. and Browning, J.L. TWEAK, a new secreted ligand in the tumor necrosis
                                                                                                                                                                                                              Submitted (14-OCT-1997) Cell Biology, Biogen, 12 Cambridge Center, Cambridge, MA 02142, USA
                                                                                                                                                                                                                                             Bourdon, P., Hession, C., Direct Submission
                                                                                                                                                                                                                                                                                       J. Biol. Chem.
98070415
                                                                                                                                                                                                                                                                                                   that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
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AF030099.1 GI:2707218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF030099
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                                                                                                                                                                                                  Location/Qualifiers
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GSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPPLNRLVRPRRSAPKGRKTR
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RPGSSLRIRTLPWAHLKAAPPLTYFGLFQVH"

247 a 434 c 388 g 257 t
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atches 929; Conservative 0; Mismarches 220; Indels 73; Gapatches 929; Conservative 0; Mismarches 120; Conserva	CCACTCTCCACCTC 9	TCCCACTCTTATCTTACAACTCCCCCACCG	CATAAATACAGTA	b 92
Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap 2 stystasgoctgagoctgagoctgagoctcgatctgagoctgagocgagoc	caactatccacctc	tccttgctcttcttaacatcccatcccacc	acagacg	83
Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap 9 gtgctggcctgggcctggcctggcctgcctgctgctgctg	ccattcc- 8 rccarccc 9	tcaaaggcagccag TCTAGAGGCTGCCTC	gtcca CTCCA	78 86
Matches 29; Conservative 0; Mismatches 200; Indels 73; Gap Matches 29; Conservative 0; Mismatches 200; Indels 73; Gap 2 gtgctgagcctgggcctgggcctggcctggcctggcctg	-getgeteett 7 AGCCGCTCTTT 8	sctacccaccccactcctccac 	ggagcate CCT	72 81
Best Local Similarity 76.0%; Pred. No. 7.6e-153; Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap 2 gtgctgagcctgggcctggcctggcctggcctggcctgg	ctttccctggctcc 7 accreccecrcc 8	tgaggggccttgctctcccagattcctta 	tettteaag TCTTCCAGO	66 75
Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap 2 gtgctgagcctgggcctgggcgtggcctggcctggcctg	taacctactttgga 6 TCACCTACTTCGGA 7	ctcatcttaaggctgccccttc 	ggatccgca GGATCCGCA	69
Best Local Similarity 76.0%; Pred. No. 7.6e-153; Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap 2 gigctgagcctgggcctgggctggcgctggcctggcctgg	റെ ന	glyccagytytctygyctyttyccyctycyg 	cccagctccgtt CCCAGCTCCGCC	6 4
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Best Local Similarity 76.0%; Pred. No. 7.6e-153; Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap 11111111111111111111111111111111111	aac 4 GAT 5	Lgatgaggaaaggctgtctacctgaagctg 	tgtcaggtgcactt TGTCAGGTGCACTT	42 51
Best Local Similarity 76.0%; Pred. No. 7.6e-153; Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap 2 gtgctgagcctggcctggcctggcctggcctggcctggc	ctgtac 4	jattggggaatttacagtcatcagggctgggc 	gctac GCTAC	3 6 4 5
Best Local Similarity 76.0%; Pred. No. 7.6e-153; Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap 2 gtgctgagcctggcctggcgctggcctggcctggcctgctgctgctg	ctccagccctctg 3 CTCCAGCCCTCTG 4	ngtgagtggctgggaagagaccaaaatcaaca 	gtgtggat grgrggac	39
Best Local Similarity 76.0%; Pred. No. 7.6e-153; Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap details 929; Conservative 0; Mismatches 220; Indels 73; Gap 11111111111111111111111111111111111	ggagcacaagca 3 GGAGCGCAGGCA 3	pattatgaggttcatcctcggccaggacaç 	gagctattgcagc GAGCGATCGCAGO	33
Best Local Similarity 76.0%; Pred. No. 7.6e-153; Matches 929; Conservative 0; Mismatches 220; Indels 73; Gapmatches 929; Conservative 0; Mismatches 220; Indels 111111111111111111111111111111111111	ggcctcgc 2 GGCTCGA 3	ctcgaagaagtgctc 	aaca + + ACC	18 27
Best Local Similarity 76.0%; Pred. No. 7.6e-153; Gap Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap Matches 929; Conservative 0; Mismatches 220; Indels 73; Gap Conservative 0; Mismatches 220; Indels 7	tggtacctttc 1 CTGCGCCTTTC 2	Lgaactgaatccccagacagaggaaagccagg 	gccggg Accage	12
Best Local Similarity 76.0%; Pred. No. 7.6e-153; Matches 929; Conservative 0; Mismatches 220; Indels 73; Gaps 2 gtgctgagcctggcctggcgctggcctgcctggcctggc	acagcagaggac 1 GTGGCAGAGGAG 2	gctgtctgcccaggagccttctcaggaggagc 	ggaget GGAGCO	15 6
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                                  synthetic construct.
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Sequence 1 :
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AX180714.1
Tweak receptor
Patent: WO 0145730-A 1 2
IMMUNEX CORPORATION (US)
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KIYHIENEIARTIKKLIGERTRSSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEEES
QDPAPFLNRLVRPRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEA
RINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEE
FSATAASSLGPQLRLCQVSGLLALRPESSLRIRTLPWAHLKAAPFLTYFGLFQVH"
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               773
                                         358
                                                                  713
                           tctgcgctacgaccgccagattggggaatttacagtcatcagggctgggctctacct 417
               TCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCT
                                                                                                                         685;
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                                                                                                                                     Similarity
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agcaggtgtggatgggacagtgagtggctgggaagagaccaaaatcaacagctccagccc 357
ACCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCC 772
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Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Submitted (07-DEC-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Tratitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.govseries: IRAL Plate: 30 Row: p Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4507596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: nisc_mgc@nhgri.nih.góv
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete cds.
BC019047
BC019047.1 GI:17512138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaithersburg, Maryland; Web site: http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL:
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                                                                                                                                                                                                                                                                                             /translation="MAARRSQRRRGERPGTALLVPLALGLGLALACLGLLLAVVSL
GSRASLSAQEEAUVAEEDODPSELMPQTEESQDPAPFLNRLVRPRRSAPKGRKTR
ARRALAAHYEVHPRPGQDBAQADGGVTTCLRP"
1 309 t
                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"Similar to tumor superfamily, member 12" /protein_id="AAH19047.1" /db_xref="GI:17512139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:20669 IMAGE:4766071"
/tissue_type="Primary B-Cells fro
/clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Vector: pOTB7"
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73.7%;
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Primates;
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                                                                                                             Score 409.4; DB 9;
Pred. No. 1.8e-96;
0; Mismatches 171;
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Catarrhini; Hominidae;
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                          AUTHORS
TITLE
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                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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AC016876.4 GI:15421989
HTG; HTGS_PHASE1; HTGS_I
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                                Homo
                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                             sapiens
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baldwin,J., Barna,N., Beckelly,R., Boguslavkiy,L., Boukhgalter,B.,

Brown,A., Castle,A., Colangelo,M., Collins,S., Collynore,A.,

Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,

Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,

Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,

Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,

McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,

Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 181928 bases at least Q40
Consensus quality: 18529 bases at least Q40
Consensus quality: 187335 bases at least Q40
Consensus quality: 187335 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 188058; sum-of-contigs
Quality coverage: 8.1 in Q20 base; agarose-fp
Quality coverage: 7.2 in Q20 base.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 16 contigs. The true order of the pleces
**is not known and their order in this sequence record is
**arbitrary. Gaps between the contigs are represented as
**runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence
**a soon as it is available and the accession number will
**be preserved.
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All repeats were identified thing RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-DEC-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 3, 2001 this sequence version replaced gi:13431059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L3849
Center clone name: 186_B_7
Center clone name: 186_B_7
Sequencing vector: M13; M77815; 3% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
58981
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346 47136: contig of 6291 bp
37 47236: gap of 100
37 58980
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100 t

35121: gap of 100 k

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CAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGT
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116865 136408: contig of 19544 bp in length
136409 136508: gap of 100 bp
136509 156380: contig of 19872 bp in length
156381 156480: gap of 100 bp
156481 18631: contig of 24151 bp in length
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20804. .21935
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68265. .94625
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35122. .40745
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22036. .24202
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/db_xref="taxon:9606"
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                               179030 bp DN. Rattus norvegicus clone CH230-154B15, ***, 68 unordered pieces.
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PROGRESS
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REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus (bases 1 to 179030)

SOURCE ORGANISM

Rattus norvegicus Norway rat.

AC098923.4 GI:17 HTG; HTGS_PHASE1.

GI:17973852

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Garter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Dellaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinih, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcala, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Harniston, K., Harris, K., Hart, M., Havlander, O., Harris, K., Hart, M., Havlander, M., Hollows, C. Hollins, B., Homsi, F., Hernandez,J., Hernandez, O., Howard, S., Hodgson, A., Hogues, M., Holloway, C.,

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TITLE
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TITLE
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Direct Submission
Submitted (06-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
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                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 68 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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be
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                                                                                                                                                                                                                                                                                         Consensus quality: 137096 bases at least Q40 Consensus quality: 145080 bases at least Q30 Consensus quality: 152950 bases at least Q30 Estimated insert size: 138980; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 0.990329First call
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
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Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;

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REFERENCE AUTHORS Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Galil, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hully, S., Hume, J., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Luna, R., Luna, Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mapua,P., M (bases 1 to 118395) Martin, Martindale, A.

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Baylor Plaza, Houston,
On Dec 20, 2001 this se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.990329First call findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draff_data.html).
NOTE: This is a 'working draff' sequence. It currently consists of 68 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dec 20, 2001 this sequence version replaced gi:16756150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 85618 bases at least Q40 Consensus quality: 94111 bases at least Q30 Consensus quality: 9937 bases at least Q20 Estimated insert size: 55807; sum-of-contigs estimation quality coverage: 0x in Q20 bases; agarose-fp estimation
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Center clone name: CH230-191M14
----- Summary Statistics
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Center code: BCM
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Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L. Direct Submission
Submitted (05-0CT-2001) Psychiatry, Johns Hopkins Medical
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/gene="JPH3"
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/gene="JPH3"
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HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
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/protein_id="AAL40941.1"
/db_xref="GI:17646245"
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/db_xref="taxon:9606"
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Pred. No. 0.0017;
8; Mismatches 240;
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                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.990319
Consensus quality: 184004 bases at least Q40
Consensus quality: 184151 bases at least Q30
Consensus quality: 184222 bases at least Q30
Consensus quality: 184222 bases at least Q30
Consensus quality: 184222 bases at least Q20
Insert size: 18157; agarose-fp
Insert size: 185622; sum-of-contigs
Quality coverage: 12.8x in Q20 bases; agarose-fp
Quality coverage: 12.8x in Q20 bases; sum-of-contigs.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 3 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.

**This record will be updated with the finished sequence
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Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Abola,A.P., Bruno,D., Gonn,L., Dela Rosa,M., Faulkner,D.,
Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,G.J.,
Mao,J., Wilhelmy,J., Yu,S. and Davis,R.W.
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On Dec 22, 2000 this sequence version replaced gi:11908285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-JUN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Homo sapiens chromosome 1 clone RP11-54C13, WORKING DRAFT SEQUENCE,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: 956
Center clone name: RP11-54C13
Center clone name: RP11-54C13
                                                                                                                         24946
25046
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                               1. .185822
                                                                                     Location/Qualifiers
                                                                                                            24945: contig of 24945 bp in length
25045: gap of unknown length
66297: contig of 41252 bp in length
66397: gap of unknown length
185822: contig of 119425 bp in length
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/notee"assembly_name:Contig9"
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/note="assembly_name:Contig8
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/clone_lib="RPCI human BAC library 11"
1. .24945
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                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1353)

Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V Stone,D.M., Watanabe,C.K. and Wood,W.I.

Compositions and methods for the treatment of tumour Patent: WO 0153486-A 3 26-JUL-2001;
                                                                     Genentech,
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Sequence 3 from Patent w00153486.
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/map="17p13"
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Apo3/DR3"
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TWEAK, a new secreted ligand in the t
that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410
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Mammalla; Eutheria; Primates;
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Chicheportiche,Y., Bourdon,P.R
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                         /translation="MAARRSQRRRGERGEPGTALLVPLALGLGLALACLGLLLAVVSL GSRA,SLSAQEPAQEELVAEEDQDPSELMPQTEESQDPAPFLRRUVRPRRSAPKGRKTR ARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGL YYLYCQVHPDEGKAVKLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH"

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/db_xref="taxon:9606"
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Pred. No. 6e-2
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No. 6e-204;
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Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 1651)
                                                                                                      Homo sapiens, superfamily,
                                                                                complete cds.
BC019047
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                                                                     BC019047.1 GI:17512138
                                               human.
                                                                                                     Similar to tumor nember 12, clone I
           Chordata;
Primates;
                                                                                                    1651 bp mRNA
to tumor necrosis
clone MGC:20669
           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                    linear PRI factor (ligand) IMAGE:4766071, π
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Tissue Procurement: Louis Staudt
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov Series: IRAL Plate: 30 Row: p Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507590 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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Contact: MGC help desk
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superfamily, member 12"
/protein_id="AAH19047.1"
/do_xref="Gi:17512139"
/translation="MAARRSQRRRGERGEPGTALLVPLALGIGIALACLGILLAVVSL
GSRASISAOEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR
ARRAIAHYEVHPRPGQDGAQADGGYTTCLRP"
a 517 c 481 g 309 t
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/db_xref="taxon:9606"
/clone="MGC:20669 IMAGE:4766071"
/tissue_type="Primary B-Cells fro
/clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"
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                          actococoacogcocoactctocacotcactagotcocoaatcocotgacoctttgaggoco
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
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Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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Liehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maddrim, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
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ACO16876.4 GI:15421989
ACO16876.4 GI:15421989
TOO UTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: 186_B_7
Center clone name: 186_B_7
Center clone name: 186_B_7
Sequencing vector: M13; M77815; 3% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 181928 bases at least 040
Consensus quality: 18529 bases at least 030
Consensus quality: 187335 bases at least 020
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NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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58981 59080: gap of 100 bp

59081 68164: contig of 9084 bp in length

68165 68264: gap of 100 bp

68265 94625: contig of 26361 bp in length

94626 94725: gap of 100 bp

94726 102564: contig of 26361 bp in length

94726 102564: contig of 7639 bp in length
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20803: gap of 100 bp
20804 21935: contig of 1132 bp in length
21936 22035: gap of 100 bp
22036 24202: contig of 2167 bp in length
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35122 .40745
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/db_xref="taxon:9606"
/clone="RP11-186B7"
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gtggatggtgtgctggcctgcgctgcctggaggaattctcagccactgcggccagttcc
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                                                                                 GTGGATGGTGCTGCCCTGCGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCC
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/protein_id="CAC50004.1"
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/protein_id="GI:1513571"
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/the control of the control
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/db_xref="taxon:32630"
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TTGGAACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCGGAAGGCGCGGCCTCGC
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TWEAK, a new secreted ligand in the tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
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GYLALRCLEEFSATAASSPGPQLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Netzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferragutto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J. H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mel, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley,K.C.
Direct Submission
Submitted (31-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 25, 2001 this sequence version replaced gi:12621364.
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Web site: http://www.hgsc.bcm.tmc.contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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Location/Qualifiers
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62252: gap of unknown length
118772: contig of 56520 bp in 10
118872: gap of unknown length
148924: contig of 30052 bp in 10
149024: gap of unknown length
167331: contig of 18207 bp in 10
167331: gap of unknown length
189907: contig of 2576 bp in 10
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                                                                                                                                                                                                                                                                                CCGACCACGTGTTTATTGACTTTGTGCAC
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                                                                                                                                 gtggatttttaaaacagatattattttttattattattgtgacaaaatgttga
                                                                                                                                                                                                                                                                                                                                                                                       GA----CGTATCCTTGCTCTTTTAACATCCCATCCCACCACAACTATCCACCTCACT
                                                                                                                    GTGGATTTTGAAA---AGATACTATTTTATTATTATTGTGACAAAATGTTAA
                                                                                                                                                                        AGAAGTTCCCAACTGTGAGGGGGAAGAGCTGGGGGACAAGCTCCTCCCTGGA----TCCCT
                                                                                                                                                                                      aggagttcccaaatgtgaggggcgaga-aacaagacaagctcctcccttgagaattccct
                                                                                                                                                                                                                           -- CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGACTAGGCC
                                                                                                                                                                                                                                        ttcaggcactaagagggctggacctggccggcaggaagccaaagagactgggcctaggcc
                                                                                                                                                                                                                                                                                                       acccccagggcattgtgttcactgtactctgtgggcaaggatgggtccagaagaccccac 1195
                                                                                                                                                                                                                                                                                                                                   AGCTCCCAAAGCCCCTACTTATC-----
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                                      Mouse DNA sequence
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/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-168P5"
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                            ttccaggttcactgaggggccctggtctccccacagtcgtcccaggctgccggctcc---
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers giver in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Nov 20, 2001 this sequence version replaced gi:16605765. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxto Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-422L16 from the RPCI-23 Mouse PAC Library
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complement(84050, .84131)
/note="Sequence from uni-directional primer reads and dGTP
big dye terminator reads only."
a 56824 c 57519 g 60529 t
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RS Alabrooks, S.L., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, JR., Banks, T., Barbaria, J., Banborooks, S.L., Amaratunge, H.C., Are, JR., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Li, J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Manstin, R., Martindale, A., Monzis, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Moser, M., Neal, D., Newtson, J., Newtson, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwu,s.,
Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
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NOTE: This is a 'working draft' sequence. It currently consists of 68 contigs. The true order of the pieces is not known and their order in this sequence record is
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
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/product="junctophilin 3"
complement(<36507. .>3688
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/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
/translation="MSSGGRENFDDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWSHGFEYLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWYYKGEWTHGFKGRYGVRECAGNGAKYEGTWSNGLQDGYGTETYSDG"
32731 c 30696 g 28283 t 4254 others
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RESULT 14

DEFINITION

ACO84799 303091 bp Mus musculus chromosome 16 clone SEQUENCE, 101 unordered pieces.

DNA 1: RP23-197M9,

WORKING

HTG 17-NOV-2000

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Consensus quality: 175579 bases at least Q30
Consensus quality: 186949 bases at least Q30
Consensus quality: 186949 bases at least Q20
Estimated insert size: 198300; agarose-fp estimation
Estimated insert size: 293091; sum-of-contigs estimation
Quality coverage: 4.85 in Q20 bases; agarose-fp estimation
Quality coverage: 3.28 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 101 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary, Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Center clone name: RPCI-23_197M9
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Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
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Hollins, B., Homsi, E., Howard, S., Huber, J., Hullyk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Martinez, E., Wassey, E., Mawhiney, E., McLeod, M. P., Meador, M.,
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Morgan, M., Morris, S., Moser, M., Nickerson, E., Newtson, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Newtson, N.,
Nguyen, A., Nguyen, N., Nolas, A., Rojubokan, I., Folfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Wallas, S., Mard-Moore, S., Warren, R., Washington, C.,
Weinstock, G., and Gibbs, R.
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Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                                   NOTE: Batimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces
                                                            is not known and their order in this sequence record is
                                                                                                                                                                                                                                                Consensus quality: 21300 bases at least Q40 Consensus quality: 25175 bases at least Q30 Consensus quality: 27665 bases at least Q30 Estimated Insert size: 6068; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: CH230-12F12
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Gaps between the contigs are represented as but the exact sizes of the gaps are unknown
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1373
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                                                                                                                                                                                                                                  Description
                                         Human TREPA (TNF )
Human TNRL3 DNA.
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Mouse TNRL3 DNA.
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	AAA88730	21	813		47.6	4	
DNA encoding a mat	AAA75999	21	813		47.6	42	
Human mFLINT #1 nu	AAZ25377	20	813		47.6	41	
Human APO6 DNA. H	AAX23419	20	767		47.6	40	
Human adenosine Al	AAX53491	20	114955	3.5	48	39	
Micromonospora DNA	AAS08693	22	109519	3.5	48	38	
۲,	AAA38185	21	320	3.5	48	37	a
portic	AAN70194	80	201		48.8	36	
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##	AAZ25376	20	936		49.2	27	
mature	AAA51078	21	825		•	26	
**	AAZ25378	20	825	3.6	49.2	25	
cDNA encoding huma	AAA72028	21	1517		49.6	24	
a	AAZ77506	20	2188	3.6	50	23	
Streptomyces prote	AAN70195	æ	201		50	22	
PRO207	AAA49732	21	50	3.6	50	21	
tumour necr	AAX56002	20	50		50	20	
PKD1 locus	AAT94108	19	53577		53.2	19	
poly	AAT18551	17	53577		53.2	18	
	AAT94101	19	53526		53.2	17	
	AAA02504	21	1593	4.0	54.4	16	o
n colon can	AAA02488	21	1218	4.2	58	15	o
æ	AAA10594	21	10732	4.3	59.2	14	o
colo	AAA02484	21	1000	4.4	60.6	13	o
gene expr	AAZ17263	20	_	4.4	61	12	
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Human gene signatu	AAT22190	16	282	17.9	245.4	10	

ALIGNMENTS

RESULT AAV18600 18-MAR-1997; 07-AUG-1996; 18-OCT-1996; CDS TRELL; tumour necrosis factor related ligand; tnf; treatment; cancer; autoimmune disease; immune system; stimulation; suppression; graft rejection; ds. 07-AUG-1997; 21-JUL-1998 (first entry) AAV18600; AAV18600 standard; cDNA; 1373 (BIOJ) BIOGEN INC. 12-FEB-1998 WO9805783-A1 Homo sapiens Homo sapiens tumour necrosis factor related ligand (TRELL) gene 97US-0040820. 96US-0023541. 96US-0028515. 97WO-US13945 Location/Qualifiers
1..852 /note= /*tag= a "tumour necrosis factor related ligand" ВР

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Best Loc
Matches
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                                             CDNA clone DNA30879-1152
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antitumour; tumour; therapy; cytostatic;
ovarian cancer; renal cancer; colorectal
; prostate cancer; lung cancer; bladder cancer;
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(ANTCC 209358) encoding human pRO207 (see AAY95338), which shows commology to several members of the tumour necrosis factor family, especially human lymphotoxin (23.4%). The cDNA was identified in a feetal kidney cDNA library following identification of an expressed sequence tag with homology to human Apo-2 ligand. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumour cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO319, PRO310, PRO526, PRO326, PRO320, PRO320 or PRO866 (see AAY95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, covarian, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Nucleic af the antitumour no lucentiace
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Best Loc
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                                                      composition to inhibit neoplastic cell growth or in mammal comprises polypeptides PRO179, PRO207, 1, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, 6
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                                                     The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, also to induce apoptosis for treating cancer and eliminating autoreactive T cells, as an adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can also be used to target cytotoxic agents or for affinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more responsive to TREPA and to screen for TREPA mimics. Ribozymes, antisense RNA, antibodies or peptides, are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting vascularisation), inflammation or a wide range of autoimmune conditions, conditions involving abnormal entirelation of colleges to the conditions.
                     vascularisation), inflammation or a wide range of autoimmune conditions involving abnormal stimulation of epithelial cells atherosclerosis), for birth control (inhibiting ovulation and formation) or other angiogenic conditions (e.g. ulcers).
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                                       The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present sequence is a cDNA clone ID #690050 encoding human TREPA.
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This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic moiety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or expressed on the cell surface. The binding is preferably performed in vivo. APO4 polypeptides/active fragments are also useful for screening for agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or
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RESULT
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            The sequence represents a DNA from the expression vector pDC409-LZ-TWEAK, which encodes a fusion protein comprising a growth chormone leader, a leucine zipper multimerisation domain, and the extracellular domain of human TWEAK. The fusion protein was used in the isolation of human TWEAK receptor (TWEAKR)-expressing clones commber of the tumour necrosis factor (TNE) family and induces and develop comment of the tumour necrosis factor (TNE) family and induces and glogenesis. TWEAKR may therefore be used to screen for and develop commented by angiogenesis include ocular disorders characterised by coular covascularisation such as diabetic retinopathy, neovascular glaucoma, retinopathy of prematurity, retrolental fibroplasia, corrected to uveitis, macular degeneration and corneal graft cheovascularisation, and inflammatory diseases include malignant and corneatism and psoriasis. Other treatable diseases include malignant and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions such as sarcomas and carcinomas, benign tumours and conditions conditions such as sarcomas and carcinomas, benign tumours and conditions conditions carcinomas conditions carcinomas conditions carcinomas conditions carci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treat, suppress or alter immune responses (especially involving human adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for screening natural/synthetic DNAs for TRELL-encoding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon-gamma, to induce cell death or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligand (TRELL). TRELL or active fragments can be included with carrier in pharmaceutical compositions to treat cancer, autoimments of the control of the con
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                                                                                                                                                                                                                                                                      This invention describes isolated Tumor Necrosis Factor (TNF) family Creceptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 is useful for identifying prostate cancer concerts determining levels of APO4 is useful for identifying selective by determining apents, useful in diagnosis/treatment of disease by binding of agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC in agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vitro. APO9 polypeptides are also useful for diagnosis/treatment of developmental or gestational also cuseful for diagnosis/treatment of developmental or gestational cell line (MEP-7, and induced aponesses).
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Best Local
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P-PSDB; AAW93591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal ceil function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
                                                                                                                                                                                                                                     pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1290
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17-SEP-1998;
                                                                                                                                                                                       hepatocellular carcinoma; prostate cancer; ss.
                                                                                                                                                                                                                                                                                                            acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                             impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic
                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX53491
                                             25-MAR-1999
                                                                                           W09913886-A1
                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caaggatgggtccagaagaccccacttcaggcactaagaggggctggacctg-gcggcag
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98WO-US19419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.9%;
97.3%;
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                                                                                                                                                                                                              kidney
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                                                                                                                                                                                                                 cancer;
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                                                                                                                                                                                                                 melanoma;
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Conservative

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Mismatches 316;

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VGGCCVGCGNNHNNNSCCVGGCCVGCGNNHNNNSCCCVGGCCVGCGGNNHNNNSGCCC CGGCGCGCCCVGGCCVGCGNNHNNNSGGCCVGCGGNNHNNNSVGGCCVGCGGNNHNNNSC

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gggagccgggcaccgccctgctggtcccgctcgcgctgggcctgggcctggccttggcctt CGGCGGCGCCCNNHNNNSCGGCCCGGCCGCGCGCGCCCVNNHNNNSCGGCCCGGCC aggcacagccccccccccatggccgcccgtcggagccagaggcggaggggggcgcggg CCGGCCGGCGCGCNNHNNNSCGGCCCGGCCGGCGCGCCCNNHNNNSCGGCCCGGC

GGCGGCGCCCVGNNHNNNSCGGCCCGGCCGGCGGCGCCCVGGNNHNNNSCGGCCCCG

105152

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gtgcacctaaaggccggaaaacacgggctcgaagagcgatcgcagcccattatgaagttc CCVGNNHNNNSCGGCCCGGCCGGCGCCCCVGGCCVGCNNHNNNSCGGCCCGGCCGG agacagaagaaagccaggatcctgcgcctttcctgaaccgactagttcggcctcgcagaa CGGCCCGGCCGGCGCGCCCVGGCCVNNHNNNSCGGCCCGGCCGGCGCGCCCCVGG agcctgcccaggaggagctggtggcagaggagcaggacccgtcggaactgaatcccc GCCGGCGGCGCCCVGGCNNHNNNSCGGCCCGGCCGGCGGCGCCCCVGGCCNNHNNNS QΥ В οy 밁 Ş

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Matches 182;
                  Query Match
Best Local Similarity
                                                                                                                                       may be derived from sequences AAX5272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, beast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-1998;
17-SEP-1997;
                                                                                                           Sequence 114955 BP; 6071 A; 29417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 37; 120pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0093972
97US-0059160
                5.1%;
                  Score 70.4; DB 20; Pred. No. 2.7e-05;
                                                                                                         C; 36712 G;
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                                                                                                           21328 т;
                                       Length
                                                                                                           21427 other;
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The present invention describes a library of human polynucleotides CC comprising the sequences given in AAZ12532 to AAZ1779. Also described is CC a method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell CC suspected of being cancerous, where the gene product is encoded by one CC polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, CC mapping, tissue typing or profiling, forensics, genetic analysis and CC detection of polymorphisms. Polypeptides encoded by the polynucleotides CC can be used for raising antibodies for experimental, diagnostic and CC therapeutic purposes. The polynucleotides may also be used to construct CC arrays for diagnostics (which may be used to detection of expression levels between CC cells (e.g. to identify abnormal or diseased tissue in a human, to CC two cells (e.g. to identify abnormal or diseased tissue in a human, to cidentify a genetic predisposition or susceptibility to a disease such as CC diagnostis, prognosis and management of colorectal cancer, breast cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104792
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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(HYSE-)
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Escobedo J, Garcia PD,
Jones WL, Kassam A, Ke
Lamson G, Leshkowitz D,
                                                                                                                                                                                                                                                                                                                                                                  Novel human genes and their expression products which differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1999
                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stache-Crain
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HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                     A, Dickson M, Dime
Garcia PD, Garcia V, Giess
(assam A, Kennedy GC, Kita D, Lauge
(assam A, Kennedy GC, Kita D, Lauge
Randazzo F, Reinh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression product; diagnosis; therapy; probe;
apping; tissue typing; profiling; forensic; cancer;
ysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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''a V, Giese K, Inhı..
''a D, Labat I;
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Query Match
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Matches 145
                 14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                           AAA02484 standard; cDNA; 1000
                                                                                                                                                                                                                                                                                                                                                  1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and lung cancer. The polynucleotides can also peptide analogues and antagonists.
                                                                                                                                           Homo
                                                                                                                                                              oestrogen
                                                                                                                                                                         breast cancer;
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                                                                                                                      WO9958675-A2
                                                                                                                                                                                probe;
                                                                               13-MAY-1999;
                                                                                                  18-NOV-1999
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98US-0105877.
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98US-0085537
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Matches 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes correlated with a cancerous state of a mammalian cell, comprisin detecting at least one differentially expressed gene product in a test
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Reinhard C, Giese K,
Lamson G, Drmanac R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1000 BP;
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Similarity
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Crkvenjakov R,
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R, Dickson M,
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Stache-Crain B;
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V, Drmanac S, Lak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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(OJIP ) OJI PAP
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 ACSTYASTDNCSRSRTTSTCYTAKYSYSTBSTNCYSDSRGSDNSTAKYASTTTYDAYDAR
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            WO9958675-A2
                                                                                 breast
                                                                                                                                     Human colon cancer cell line
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                                      Homo sapiens
                                                                  oestrogen receptor-negative
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                                                                             cancer; oestrogen receptor-positive breast cancer; therapy,
                                                                                          colon cancer; tumour; diagnosis; gene expression produc detection; cancerous state; metastasis; identification;
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                                                                  breast cancer; lung cancer;
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15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                            1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                          negative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        breast cancer, lung
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Randazzo F, Kennedy GC, F
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Garcia V, Jones LW, Stac
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gb_est2:B1871711
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Query: US-09-245-198A-4
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-Q=/cg12_1/USPTO_spool1/US09245198/runat_21062002_184006_9934/app_query.fasta_1.632
-DB=EST -QBMT=fastap - SUFETX=TS - GAPOD=12.000 - CAPEXT=4.000
-MINMATCH=0.100 - LOOPCL=0.000 - LOOPEXT=0.000 - PGAPOD=6.000
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                                                                                                                                              LeuAlaLeuAlaCysLeuGlyLeuLeuLeuAlaValValSerLeuGlySe
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Length: 221
Gaps: 1
Percent Identity: 99.095

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gb_est2:BI734016
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI2034 row: b column: 07
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                 High quality sequence stop:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NHH_MGC Library."

a 242 c 228 g 136 t
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/clone_lib="NIH_MGC_90"
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/db_xref="taxon:9606"
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5 HS_3054_A1 H03 MF C
4 602638308F1 NIH_MGC.
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                                                                                                                                                                                                                                                                                                                                                               gb_est2:BI870393
                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 728)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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BI870393.1 GI:16044066
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                                                                                                                                         Contact: Robert Strausberg, Ph.D
                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                  mRNA sequence.
                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12034 row: a column: 12
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                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
quality sequence stop:
Location/Qualifiers
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cDNA clone IM
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214 LeuAspLeuLeuValAspGlyValLeuAlaLeuArgCysLeuGluGluPh
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Site_2: SalI: Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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AUTHORS
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                                 uPheGlnValHis 284
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BI819200
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EST.
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Tissue Procurement: Life Technologies, Inc.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Plate: LLAM11437 row: l column:
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                                                                                                                                                                                                                                                                                                                    Gruber (Invitrogen). Research Genetics tracking 021. Note: this is a NIH_MGC Library." 268 c 215 g 154 t
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seq_documentation_block:
LOCUS BI766766
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11517 row: c column: 18
High quality sequence stop: 772.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                    ArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerLeuGlyProGl
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                    erLeuArgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPhe 274
                                                                                                nLeuArgLeuCysGlnValSerGlyLeuLeuAlaLeuArgProGlySerS
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CCCTGCGGATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCTTC
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/clone_lib="NIH_MGC_122"
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                                                                                                                                             105 GluLeuAsnProGlnThrGluGluSerGlnAspProAlaProPheLeuAs
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11722 row: k column: 13
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria;
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Percent Identity: 99.444
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Site_2: SalI; Cloned unidirectionally. Primer: Average insert size 1.6 kb. Constructed Life Technologies. Note: this is a NCI_CGAP Library." a 292 c 268 g 204 t I others

Primer: Oligo

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SOURCE
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LOCUS BF577781
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NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (M National Institutes of Health, Mammalian Gene Collection (M Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM9767 row: p column: 20
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High quality sequence start: 17
High quality sequence stop: 724.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4206595"
/clone=11b="NCI_CGAP_CO24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPOR
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                                                                                        musculus"
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283 lHis 284
                                       AlaHisLeuLysAlaAlaProPheLeuThrTyrPheGlyLeuPheGlnVa
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| ACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGCAGAGGACC
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Other_ESTs: ur70d09.x1
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria;
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Location/Qualifiers
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/clone="IMAGE:3155633"
/clone_1ib="NCL_CGAP_Mam3"
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4.609
95.722
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/dev_stage="10 months"
/lab_host="DH10B"
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VERSION
KEYWORDS
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LOCUS BI762908
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                                                                                                                                                                                                                                                                                                                       National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                     Email: cgapbs remail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST.
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                                                                                                                       quality sequence stop: 647.
Location/Qualifiers
                                                                                                                                                            LLAM11470 row: c column:
                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5188168"
/clone_lib="NIH_MGC_116"
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141 AlaIleAlaAlaHisTyrGluValHisProArgProGlyGlnAspGlyAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 nProGlnThrGluGluSerGlnAspProAlaProPheLeuAsnArgLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 TGGTCGTGGTCAGCCTGGGGAGCTGGGCAACGCTGTCTGCCCAGGAGCCT 150
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                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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alignment_scores:
    Quality:
    Ratio:
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Val.SerGlyTrpGluGluAlaArgIleAsnSerSerSerProLeuArgT 181
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alignment_block: US-09-245-198A-4

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BG686319

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KEYWORDS
SOURCE
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   Quality:
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ORIGIN
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  Percent Similarity:
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BG686319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1625 row: p column: 08
High quality sequence stop: 587.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602638232F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766071 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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                       Ratio:
                                                                                                                                                                108
                                                                                                                                                      /clone_lib="NIH_MGC_48"
//clone_lib="NIH_MGC_48"
//tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)", Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
738.00
4.855
97.436
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4766071"
  Percent
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Gaps: 2
Identity: 97.436
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                                                                                               Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new (Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                    Carninci, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama, RiKEN Gemomic Sciences Center (GSC), Tsurumi-ku, Yokohama, RiKEN Yokohama, RiKEN Yokohama, RiKEN Yokohama, RiKEN Yokohama, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc:riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc:riken.go.jp/, Tel:81-45-503-9222, Riken.go.jp/, Riken.go.jp/, Riken.go.jp/, Riken.go.jp/, Riken.go.jp/, Riken.go.jp/, Riken.go.jp/, Riken.go.jp/, Riken.go.jp/, Rik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI Host: DH10B. Retina RNA was provided by Stefano Gustincich (Department of Neurobiology, Harvard Medical School, Longwood Ave., Boston, MA 02115, USA) whose assistance is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M.
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                                                                                                                                                                                                                                                                                                                                    Neurobiology, Harvard Medical School, 02115, USA) whose assistance is grate
                                                                                                                                                                                                                                                                                                                                                                       Retina RNA was provided by Stefano Gustincich (Department
Neurobiology, Harvard Medical School, 220 Longwood Ave., I
                                                                                                                                                                                                                                                                                                                                                                                                                                             gratefully acknowledged.
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                                                                                                                                                                                                 /strain="C57BL,
                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                      EST348878 Rat gene index, normalized rat, norvegicus, Rattus norvegicus cDNA clone RGIEF49 5' end, mRNA sequ
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300 c 248 g 256 t 1 others
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CysGlnValHisPheAspGluGlyLysAlaValTyrLeuLysLeuAspLe 216
                                                                                                                                                                                                                                                                             rgGlnIleGlyGluPheIleValThrArgAlaGlyLeuTyrTyrLeuTyr 199
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Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlayage,A.R. and Adams,M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research 9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
Contact: Lee, NH
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96.296
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Xho1; Estimated insert size approx.1 kb"
188 c 147 g 138 t 3 others
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liver, embryo, heart, muscle, spleen"
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oProAlaProMetAlaAlaArgArgSerGlnArgArgArgGlyArgArgG
                                                                 ProArgSerLeuGlySerArgAspGlyGlyAlaValArgGlnAlaGlnPr 32
                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
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4.665
92.667
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LOCUS B1908274
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 894)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11546 row: d column: 08
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Tissue Procurement: Life Technologies, Inc.
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Contact: Robert Strausberg, Ph.D.
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/note-"Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                                        /clone_lib="NIH_MGC_118"
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seq_name: gb_est2:BI965174
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id34e07.y1 melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 mmsculus cDNA 5' similar to TR:043508 043508 TNF-RELATED WEAK INDUCER OF APOPTOSIS; mRNA sequence.
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                                    Align seg 1/1 to:
                                                                                                          Percent Similarity:
                                                                 US-09-245-198A-4 x BI965174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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       ProLeuProArgSerLeuGlySerArgAspGlyGlyAlaValArgGlnAl
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Tel: 617
                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brown@fas.harvard.edu)
                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617-495-1812
                                                                                                                                                                                                              78
                                     в1965174
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                                                                                                          645.50
4.421
94.194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adult, mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="ICR"
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ACCESSION
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Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
,Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI965174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing
Washington University Genome Sequencing Center For informatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Douglas Melton, Klaus H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endocrine Pancreas Consortium 
Unpublished (2000)
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Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                        and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note "Vector: psport]; Site_1: Not I; Site_2: Sal I; Fi libraries representing E10.5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cD was made by oligo-dT priming and size-selected by colum fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared support
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adult islet"
/dev_stage="Embryonic day 10.5, E12.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Both for embryonic & newborn, male for adult and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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Percent Identity:
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       85.806
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to: 474

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JOURNAL COMMENT
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VERSION
FEATURES
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                                                                                                                                                                                                                                                                                                                                           REFERENCE
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JRCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGATGTGGTACCTTTCTTGGAACAACTAGTCCGGCCTCGAAGAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rgArgGlyGluProGlyThrAlaLeuLeuValProLeuAlaLeuGlyLeu 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aGlnProProAlaProMetAlaAlaArgArgSerGlnArgArgArgGlyA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aProLysGlyArgLysThrArgAlaArgArgAlaIleAlaAlaHisTyrG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laGluGluAspGlnAspProSerGluLeuAsnProGlnThrGluGluSer 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGCCCCCCCCCATGGCCGCCCGTCGGAGCCAGAGGCGGAGGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGTGAGTGGCTGG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGCAGGTGTGGATGGG
                                                                                                                                                                                                                                                              I (bases I to 445)

I (bases I to 445)

Rarra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Geisel,S., Kucaba,T., Lacy,M., Tan,F., Underwood,K., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          vq25g07.rl Barstead
clone IMAGE:1095324
AA870722
                                                                                              WashIU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                  Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                    Theising, B., Wylie, T., Lennon, G., Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AA870722.1 GI:2966167
                                 Seq primer: -28ml3 rev2 ET from Amersham
                                                  MGI:601556
                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
quality sequence stop: 420 
Location/Qualifiers
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stromal cell line MPLRB8
5', mRNA sequence.
                                                                                                                                                     Louis,
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 GlnThrGluGluSerGlnAspProAlaProPheLeuAsnArgLeuValAr
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                 euArgLeuCysGln 246
                                                                                                                                                                                                       AlaGlyValAspGlyThrValSerGlyTrpGluGluAlaArgIleAsnSe
                                                                                                                                                                                                                                                                                                                                                                                                                  TTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTCGAAGAAGTGCTCCTAAAGGCCGGAACGG.CGGCCTCGCCGAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gProArgArgSerAlaProLysGlyArgLysThrArgAlaArgArgAlaI 142
TCCGTTTGTGCCAG
                                                                                  gCysLeuGluGluPheSerAlaThrAlaAlaSerSerLeuGlyProGlnL
                                                                                                                                     GCTGTCTACCTGAAGCTGGACTTGCTGGTGAACGGTGTGCTGGCCCTGCG
                                                                                                                                                                       AlaValTyrLeuLysLeuAspLeuLeuValAspGlyValLeuAlaLeuAr
                                                                CTGCCTGGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGGGCCCCCAGC
                                                                                                                                                                                                                                                                                                            rSerSerProLeuArgTyrAsnArgGlnIleGlyGluPheIleValThrA
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4.576
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Gaps: 0
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of: US-09-245-198A-4 to:

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Database sequences: 1736436
Database length: 858457221
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-Q=/c912_1/USPTO_spool/US09245198/runat_21062002_184008_9995/app_query.fasta_1.632
-Q=/c9n2_1/USPTO_spool/US09245198/runat_21062002_184008_9995/app_query.fasta_1.632
-DB=W.Geneseq_032802 -QFMTP-fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=4.000 -QGAPEXT=-0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPEXT=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pfs
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09245198_@CGNI_1_0 -NCPU=6 -LOCAL -OUTFMT=Dfs
-USCR=US09245198_@CGNI_1_0 -NCPU=6 -LOCAL -OUTFMT=Dfs
-USCR=US09245198_@CGNI_1_0 -NCPU=6 -LOCAL -OUTFMT=Dfs
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3.1e-90
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5.9e-83
1.1e-68
2.4e-68
3.0e-65
1.0e-61
3.76
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427.27
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seq_documentation_block:
ID AAV18600 standard:
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAS51445 - 
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:AAQ29515 + 
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:AAQ94352 + 
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH34843 +
                                       The sequence is that encoding human tumour necrosis factor related ligand (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmune diseases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon-gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for antience therapy.
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07-AUG-1996;
18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor related ligand - useful for, e.g. treating cancer, auto-immune disease and immune responses to tissue grafts {\bf r}
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(UYGE-) UNIV GENEVA FACULTY MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour necrosis factor related ligand; tnf; treatment; autoimmune disease; immune system; stimulation; suppr
                                antisense therapy
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96US-0023541.
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Sequence

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462 Ç 394 G; 270 H

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alignment_scores:
Quality: 1444.00
Ratio: 5.085
Percent Similarity: 100.000
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US-09-245-198A-4 x AAV18600
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                                                                                           GlnValHisPheAspGluGlyLysAlaValTyrLeuLysLeuAspLeuLe
                                                                                                                                                                                                                                                       erLeuSerAlaGlnGluProAlaGlnGluGluLeuValAlaGluGluAsp 100
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               CAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCT
                                                                                                                  CTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCC
                                                                                                                                                                                                                                                                                                                                                          GGCCTGCCTCGGCCTGGCCGGTGGTCAGTTTGGGGAGCCGGGCAT
                                                                                                                                                              yTrpGluGluAlaArgIleAsnSerSerSerProLeuArgTyrAsnArgG
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LeuAlaLeuArgProGlySerSerLeuArgIleArgThrLeuProTrpAl
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Gaps: 0
Identity: 100.000
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alignment_scores:
Quality: 1
Ratio:
Percent Similarity:

1377.00 5.062 97.842

Gaps: Percent Identity:

278 0 97.842

alignment_block: $US-09-245-198A-4 \times$ Align seg 1/1

ţo:

AAX56000 AAX56000

from:

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1421

GluIleSerAlaArgArgLeuProLeuProArgSerLeuGlySerArgAs

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seq_name:
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AAX56000 standard;
                  The present sequence encodes a human tumour necrosis factor (TNF) and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand cytostatic activity. Apo-3 ligand can be used to induce apoptosis in mammalian cancer cells, to induce NF-kappaB-dependent transcription at to induce JNK/SAPK-dependent responses in mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801
Sequence 1421
                                                                              Claim 18; Fig 1; 74pp; English.
                                                                                                                                  WPI; 1999-287982/24.
                                                                                                                                                     Ashkenazi AJ,
                                                                                                                                                                                             17-DEC-1997;
10-OCT-1997;
                                                                                                                                                                                                                                                22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                     Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apoptosis;
NF-kappaB-dependent transcription; JNK/SAPK-dependent response;
                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour necrosis factor Apo-3 ligand polynucleotide sequence.
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97US-0062037
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seq_documentation_block:
ID AAA49717 standard; c
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AC AAA49717;
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                                                                           /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA49717
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22-DEC-1998 08-MAR-1999 21-APR-1999 28-APR-1999 28-APR-1999 20-JUL-1999 20-JUL-1999 26-JUL-1999 15-SEP-1999 15-SEP-1999

98US-0113296. 99WO-US05028. 99US-0130232. 99US-0131445. 99US-014287. 99US-0144758. 99US-0145698. 99WO-US21090. 99WO-US21547.

02-DEC-1999; 29-JUN-2000 WO200037638-A2

99WO-US28565

CDS

/*tag= 58..177 /*tag= 1 178..804

ь מ Location/Qualifiers 58..807

mat_peptide sig_peptide

/*tag=

C

uterine cancer; central nervous

breast cancer; PRO207; human;

ovarian cancer; renal cancer; colorectal cancer; prostate cancer; lung cancer; bladder cancer;

system cancer; melanoma; leukaemia; neoplasm;

antitumour; tumour; therapy; cytostatic;

25-SEP-2000

(first entry)

PRO207 cDNA clone DNA30879-1152

Homo sapiens

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alignment_scores:
                                                                 Quality: 1366.00
Ratio: 5.097
Percent Similarity: 100.000
                                                                                The present sequence is that of cDNA clone DNA30879-1152 (ATCC 209358) encoding human pRO207 (see AAY95338), which shows homology to several members of the tumour necrosis factor family, especially human lymphotoxin (23.4%). The cDNA was identified in a foetal kidney cDNA library following identification of an expressed sequence tag with homology to human Apo-2 ligand. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO359 or PRO866 (see AAY95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Nucleic acids encoding PRO179 etc. are used in the recombinant production of the antitumour polypeptides.
                                                                Sequence
                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                             20; Fig 3; 172pp; English
                                                                BP;
                                                                 257
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 Gaps:
Percent Identity:
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            268
0
                                                                other;
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Novel composition to inhibit neoplastic cell growth or for treating tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866

WPI; 2000-442668/38. P-PSDB; AAY95338.

ΑM,

Pitti RM,

Wood

Godowski PJ, d WI;

Gurney

ΑL,

Marsters

SA;

Goddard

(GETH)

GENENTECH INC ÅJ,

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alignment_block:
US-09-245-198A-4 x AAA49717
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                                                           AlaH1sLeuLysAlaAlaProPheLeuThrTyrPheGlyLeuPheGlnVa
                                                                                                           euLeuAlaLeuArgProGlySerSerLeuArgIleArgThrLeuProTrp
                                                                                                                                                            rAlaAlaSerSerLeuGlyProGlnLeuArgLeuCySGlnValSerGlyL
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seq_documentation_block:
ID AAV47613 standard; cD
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AC AAV47613;
XX
CAAV47613;
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DT 27-OCT-1998 (first e
XX
TNF related endotheli
XX
Ss; TNF; endothelium
KW ss; TNF; endothelium
KW tissue grafting; vasc
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Homo sapiens.
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YA
Homo sapiens.
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13-AUG-1998; 98WO-U
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12-FEB-1998; 98WO-U
YA
11-FEB-1998; 98WO-U
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PD 13-AUG-1998; 98WO-U
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11-FEB-1998; 98WO-U
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PA (ABBO) ABBOTT LAB.
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PHI; 1998-447255/38.
DR
P-PSDB; AAW29745.
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PA (ABBO) ABBOTT LAB.
XX
PFT treatment of autoimmu
XX
Claim 11; Page 123-4;
XX
Detecting nucleic aci
PT treatment of autoimmu
XX
Claim 11; Page 123-4;
XX
DETECTION OF ABOUT
CC TABPA Peptides can adjunce
CC TREPA Peptides can adjunce
CC TREPA-associated dise
CC Vascularisation), inf
CC conditions involving
CC atherosclerosis, for
CC formation) or other a
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Sequence 1236 BP; 225
                                             alignment_block: US-09-245-198A-4 \times
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                                                                                                                                                                                               alignment_scores:
Align seg 1/1
                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                   T cells, as an adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can also be used to target cytotoxic agents or for affinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more responsive to TREPA and to screen for TREPA mimics, antisense RNA, antibodies or peptides, are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting
                                                                                                                                                                                                                                                                                                                                    TREPA associated diseases, e.g. tumours and metastases (by inhibiting vascularisation), inflammation or a wide range of autoimmune conditions, conditions involving abnormal stimulation of epithelial cells (e.g. atherosclerosis), for birth control (inhibiting ovulation and placental atherosclerosis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, also to induce apoptosis for treating cancer and eliminating autoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 123-4; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting nucleic acid encoding TREPA - useful for diagnosis treatment of autoimmune disease, tumours and inflammation
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                                                                                                                                                                                                                                                                                                                       formation) or other angiogenic conditions (e.g. ulcers).
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                                                                                                                  Quality: 1265.00
Ratio: 5.080
milarity: 100.000
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97US-0798692
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MetAlaAlaArgArgSerGlnArgArgArgGlyArgArgGlyGluProGl

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seq_documentation_block:
ID AAD04350 standard; cC
XX
AC AAD04350;
XX
DT 04-JUL-2001 (first 6
XX
DE Human TREPA (TNF rela
XX
KW TREPA; TNF related er
KW TREPA; TNF related er
KW grafting; vulnerary;
                                                                                                                                                       seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                          451
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            Human; tumour necrosis factor; TNF; angiogenesis; wound healing; TREPA; TNF related endothelium proliferative agent; tumour; meta
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                                               Human TREPA (TNF related endothelium proliferative agent) cDNA.
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                                                                                                                                                      /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD04350
                                                                      entry)
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             tumour; metastasis;
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alignment_block:
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Ratio: 5.080
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present sequence is a cDNA clone ID #690050 encoding human TREPA.
                                         151
                      102
                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain or tumor necrosis factor related endothelium proliferative agent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-280760/29.
P-PSDB; AAE00891.
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10-FEB-1998;
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PProSerGluLeuAsnProGlnThrGluGluSerGlnAspProAlaProP
                                         SerAlaGlnGluProAlaGlnGluGluLeuValAlaGluGluAspGlnAs
                                                                                      yThrAlaLeuLeuValProLeuAlaLeuGlyLeuGlyLeuAlaLeuAlaC
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/product= "Huma
proliferative a
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135

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seq_documentation_block:
ID AAS03964 standard; I
XX
AC AAS03964;
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                                                                                                                                                                                                                                                                  TWEAK extracellular domain; tumour necrosis factor; TNF; angiogenesis; ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; ds; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation;
                                                                                                                                                                                                             scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis; peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  651
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                                                                                                                                                                                             fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS03964
                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
/product= "Fusion protein comprising a growth hormone leader, a leucine zipper multimerisation domain, and human TWEAK extracellular
                                                                             Location/Qualifiers 52..873
                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
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alignment_block:

Percent Similarity:

US-09-245-198A-4 x AAS03964

Align seg 1/1

to:

AAS03964

from:

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898

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250 AGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGA

SerLeuGlySerArgAlaSerLeuSerAlaGlnGluProAlaGlnGluGl

94

94 uLeuValAlaGluGluAspGlnAspProSerGluLeuAsnProGlnThrG

111 299

luGluSerGlnAspProAlaProPheLeuAsnArgLeuValArgProArg GCTGGTGGCAGAGGAGCAGGACCCGTCGGAACTGAATCCCCAGACAG

 ${\tt ArgSerAlaProLysGlyArgLysThrArgAlaArgArgAlaIleAlaAla}$ AAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGC

144

399 127 349

300

alignment_scores:

Quality: Ratio:

1066.00 5.150 100.000

Percent Identity: 100.000

Length: Gaps:

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pDC409-LZ-TWEAK, which encodes a fusion protein comprising a growth control protein comprising a growth protein comprising a growth protein leader, a leucine zipper multimerisation domain, and the cextracellular domain of human TWEAK. The fusion protein was used in the isolation of human rEMEAK receptor (TWEAKR)-expressing clones of the isolation of human cDNA library. The TWEAK protein is a member of the tunour necrosis factor (TWF) family and induces member of the tunour necrosis factor (TWF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and corneal graft rubeosis, uveitis, macular degeneration and corneal graft conclusions such as sarcomas and carcinomas, benign tumours and prenepplastic conditions such as sarcomas and carcinomas, benign tumours and prenepplastic conditions, myocardial angiogenesis, heading tumours and cornerations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a DNA from the expression pDC409-LZ-TWEAK, which encodes a fusion protein co
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10-MAY-2000; 2000US-0203347
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  Sequence 898
                                       atherosclerosis, peripheral atherosclerosis and ischaemia
                                                          scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1;
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DB; AAU03499.
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  BP;
  187
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  266
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  <u>ن</u>
  178 T;
  0 other;
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                                                               coronary
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX23424
                                                                                                                                                                                                                                                                                            _documentation_block: AAX23424 standard;
                                                                                                                            CDS
                                                                                                                                                                                  Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO6; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                           244
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          (UNIW ) UNIV WASHINGTON
                            05-SEP-1997;
                                                                                     WO9911791-A2
                                                                                                                                                        Homo
                                                                                                                                                                         apoptosis; human;
                                                                                                                                                                                                                                   Human TNRL3 DNA
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                            97US-0924634
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                                                                                                               Location/Qualifiers
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/*tag= a
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301

350 193 300 176

160 201 143 151

160 200

250

CGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGC

lyValAspGlyThrValSerGlyTrpGluGluAlaArgIleAsnSerSer

GTGTGGACGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCC

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alignment_block:
US-09-245-198A-4 x
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                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                             101
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                                                                                                        hrGluGluSerGlnAspProAlaProPheLeuAsnArgLeuValArgPro
                                                                                                                                                                                                                                                                                                                       ValSerLeuGlySerArgAlaSerLeuSerAlaGlnGluProAlaGlnGl
ArgArgSerAlaProLysGlyArgLysThrArgAlaArgArgAlaIleAl
                                                                             CAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCT
                                                                                                                                                                                      GGAGCTGGTGGCAGAGGAGGACCAGGACCCGTCGGAACTGAATCCCCAGA
                                                                                                                                                                                                              uGluLeuValAlaGluGluAspGlnAspProSerGluLeuAsnProGlnT
                                                                                                                                                                                                                                                                                            GTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGA
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                 18-MAR-1997;
07-AUG-1996;
18-OCT-1996;
The sequence is that encoding mouse tumour necrosis factor related ligand (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                  Tumour necrosis factor related ligand - useful for, cancer, auto-immune disease and immune responses to
                                                                                                                                                                                              WPI; 1998-145619/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus tumour necrosis factor related ligand
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                                                                               Claim 2;
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                                                                                                                                                                                                                                   Browning JL,
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UNIV GENEVA FACULTY MEDICINE
                                                                             Pages 45-46; 69pp; English.
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96US-0023541.
96US-0028515.
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                                                                                                                  e.g. treating
tissue grafts
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| AGGAAGTGCTCCTAAAGGCCCGGAAGGCGCCCCGCCGAGCTATTGCAG
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                                                                                                                                         GGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGAAAGGCTGTC
                                                                                                                                                                                                             CCCTCTGCGCTACGACCGCCAGATTGGGGAATTTACAGTCATCAGGGCTG
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GGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGGGCCCCCAGCTCCGTT
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seq_documentation_block:
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This invention describes isolated Tumor Necrosis Factor (TNF) family Creceptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 is useful for diagnosing prostate cancer complete the polypeptides are also useful for identifying selective fragments of the polypeptides are also useful for identifying selective binding agents to the polypeptides are also useful for identifying selective complete. APO4 polypeptides are the ragment which is extracellular, or expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening composits and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments are also agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments are also agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments are also agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example VII; Fig 13B; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-205191/17.
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/product= "TNRL3"
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seq_name:

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV24140

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alignment_block:
US-09-245-198A-4 x AAX23425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transfected to human breast carcinoma cell line
                                                                     257
                                                                                                                                                                                    224
                                                                                                                                                                                                                                           207
                                                                                                                                                                                                                                                                                                   190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 701 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCF-7, and induced apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with a cytoplasmic domain of APO4 and detecting a change in level of APO4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 TTCTCAGGAGGAGCTGACAGCAGGAGCCGCGGGAGCCCCCTGAACTGA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 LeuAlaValValSerLeuGlySerArgAlaSerLeuSerAlaGlnGluPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGGTCGTCGTCAGCCTGGGGAGCTGGGCAACGCTGTCTGCCCAGGAGCC
                                                                                                                                                                                                             ValArgProArgArgSerAlaProLysGlyArgLysThrArgAlaArgAr
PheLeuThrTyrPheGlyLeuPheGlnValHis 284
                                                       erSerLeuArgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaPro
                                                                                                                oGlnLeuArgLeuCysGlnValSerGlyLeuLeuAlaLeuArgProGlyS
                                                                                                                                                                     LeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerLeuGlyPr
                                                                                                                                                                                                                                                                      AsnSerSerSerProLeuArgTyrAsnArgGlnIleGlyGluPheIleVa
                                                                                                                                                                                                                                                                                                                                                                                                      laGlnAlaGlyValAspGlyThrValSerGlyTrpGluGluAlaArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gAlaIleAlaAlaHisTyrGluValHisProArgProGlyGlnAspGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oAlaGlnGluGluLeuValAlaGluGluAspGlnAspProSerGluLeuA 107
                                          CTTCCCTTCGGATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCC
                                                                                                 CCAGCTCCGTTTGTGCCAGGTGTCTGGGCGTTTGGCGCCTGCGGCCAGGGT
                                                                                                                                                         CTGCGCTGCCTGGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGGGCC
                                                                                                                                                                                                                                                                                                                                 AACAGCTCCAGCCCTCTGCGCTACGACCGCCAGATTGGGGGAATTTACAGT
                                                                                                                                                                                                                                                                                                                                                                                        CACAAGCAGGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCGGAAGGCGCGGCCTCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCCCAGACAGAGGAAAGCCAGGATGTGGTACCTTTCTTGGAACAACTA
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4.768
96.209
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Percent Identity:
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0
89.100
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                                                                                                 550
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alignment_scores:
Quality:
                                                                                                                                                                                                                                         8×8888888
                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-245-198A-4 x AAV24140
                                                                                                                                                                                                                                                                The sequence is that of containing a BARD1 exon which can be used in the CC preparation of the recombinant breast cancer antigen, BRCA1, binding proteins BARD1, B123, BE21, BE14, BE31 or BE445, or a composition for the CC detection of a BARD1, B123, BE2, BE14, BE31 or BE445 nucleic acid sequence, specifically a wild type BARD1 composition for the detection or purification of BRCA1, useful to identify a patient having, or at risk of developing cancer. BARD1 can be used in the preparation of an anti-BARD1 antibody, and in the detection and purification of a BRCA1 protein. BARD1, B123, BE2, BE14, BE31 or BE445 can used in the citers in binding protein agonist or antagonist that alters the binding of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the binding of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or BE31 or BE445, a specific anti-BARD1 antibody can be used to identify a patient having or at risk of developing cancer.
                                                                                                                                           Ratio:
Percent Similarity:
                                                              Align seg 1/1 to: AAV24140
1788 CCCACTCGGCCAGCGGCTGGCTCTCGCGGCCCCGCCCCTGTGCCCTGCGA 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-1997;
20-SEP-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - wl
as breast cancer antigen, BRCA1, binding proteins are useful to
identify patient having or at risk of developing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; Page 307-308; 348pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-230317/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BARD1; ring protein; BRCA1; breast cancer; risk; diagnosis; exon; ss
                                                                                                                                                                                                                                       Sequence 2856 BP; 616 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TEXA ) UNIV TEXAS SYSTEM.
                14 ProLeuProArgSerLeuGlySerArgAspGlyGlyAlaVal......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bowcock AM;
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96US-0025296.
97US-0042611.
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2031..2188
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                                                                                                                                           127.00
0.836
46.769
                                                              from: 1
                                                                                                                                                                                                                                       778 C;
                                                                                                                                           Gaps:
Percent Identity:
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                                                                                                                                                                                                                                       786 G; 674 T; 2 other;
                                                              to: 2856
                                                                                                                                           325
15
25.846
                                27
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28	ArgGlnAlaGlnPro	32
1838		1887
33 1888	ProAlaProMetAlaAlaArgArgSerGlnArgArgArgGlyArgArg	48 1937
49 1938	GlyGluProGlyThrAlaLeuLeuValProLeuAlaLeuGlyLeuGlyLe	65 1967
1968	uAlaLeuAlaCysLeuGlyLeuLeuLeuAlaValValSerLeuGlySerA	82 1986
82 1987	GlnGluGluLeuValAlaGlu ::: :CCGAAGGCGGGACGATGCCG	98 2036
99 2037	pGlnAspProSerGluLeuAsnProGlnThrGluGluSerGlnAs	115 2086
115 2087	.euValArgProArgArgSer ::: \rggTcgcgGTGCCTGGGCCC	129 2136
130 2137	AlaProLysGlyArgLysThrArgAlaArgArgAlaIleAlaAlaHisTy ::: ::: ACAGTCGCGCCCCGCGCTCGACCGCCTGGAGAAGCTGCTGCGCTTCCT	146 2181
146 2182	rGluValHisproArgProGlyGlnAspGlyAlaGlnAlaGly	160 2218
161 2219	ValAspGlyThrValSerGlyTrpGluGluAlaArgIleAsnSerSer	176 2268
177 2269	SerProLeuArgTyrAsnArgGlnIle	185 2318
186 2319	GlyGluPheIleValThrArgAlaGlyLeuTyrTyrLeuT	199 2368
199 2369	yrCysGlnValHisPheAspGluGlyLysAlaValTyrLeu 	212 2397
213 2398	LysLeuAspLeuLeuValAspGlyValLeuAlaLeuArgCysLeuGluGl ::: ::: :::	229 2447
229 2448	uPheSerAlaThrAlaAlaSerSerLeu.GlyProGlnLeuArgLeuCys	245 2497
246 2498	GlnValSerGlyLeuLeuAlaLeuArgProGl::::::::::::::::::::::::::::::::::::	256 2547
256 2548	ySerSerLeuArgIleArgThrLeuProTrpAla. :::	267 2594
268 2595	HisLeuLysAlaAlaProPheLeuThr ::: GCGGGCCGCCCGGAGACCCTCTAAATTAGAAGCAGCTGCCACTCTAAGT	276 2644

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seq_documentation_block:
ID AAA49205 standard; cDNA; 1660 BP.
XX
AC AAA49205;
XX
DT 12-DEC-2000 (first entry)
XX
DE Corn putative lecithin:cholesterol
XX
KW Corn; lecithin:cholesterol acyltran
XX
OS Zea mays.
X
                                                                                                                                       alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
                                                                                          alignment_block:
US-09-245-198A-4 x AAA49205
                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA49205
                                                              Align seg 1/1 to: AAA49205
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                                                                                                                                                                                                                                                                              The present sequence is a putative coding sequence for a corn lecithin:cholesterol acyltransferase (also known as phosphatidylcholine-sterol O-acyltransferase). This enzyme is found associated with high-density lipoproteins and Apolipoprotein-Al and -D. The gene and protein can be used to produce transgenic plants which have increased lipid metabolism and membrane fluidity, and therefore increased resistance to heat and/or cold shock, to alter the content of phytosterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
CDS
394 CAACGAGTACCGGAACCTCGCCGG.....CGTCGAGACGCGAGTGCCCA 437
                                                                                                                                                                                                                                      Sequence 1660 BP;
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 43-44; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding plant lecithin:cholesterol acyltransferase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cahoon RE, Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999;
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phosphatidylcholine-sterol 0-acyltransferase; heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corn putative lecithin:cholesterol acyltransferase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                               libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E
                   lecithin in grains and to identify potential herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-412337/35.
DB; AAB01210.
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                                                                                                                                          126.50
0.866
45.768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "lecithin:cholesterol acyltransferase"
/EC_number= "2.3.1.43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 77..1396
                                                                                                                                                                                                                                      361 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakai H,
                                                                                                                                                                                                                                      475 C; 499
                                                              from: 1
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                                                                                                                                        Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shen JB,
                                                            to: 1660
                                                                                                                                                                                                                                      G; 325 T; 0 other;
                                                                                                                                        : 319
: 17
: 25.392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat shock; cold shock; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saylor JJ;
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27	1ArgGlnAlaGlnProProAlaPro	36
438	AGAGCCTTCAGCCACAAGAACCCCCTCAAGTCAGA	487
36 488	OGly GAGA	52 537
53	alProLeuAlaLeuGlyLeuGlyLeuAlaLe	67
538	CGGAGCCCCTACGACTTCCGCTACGCGCCGT	587
	AlaCysLeuGlyLeuLeuLeuAlaValValS	78
588	CGAGGTGTACTCCCGCTACTTCAAGGAGCTGATG	637
7	LeuGlySerArgAlaSerLeuSerAlaGlnGluProAlaGlnGluGlu	94
638	AGCTGGTCGA	648
95	alAlaGluGluAspGlnAspProSerGluLeuAsnProGlnThrGl:::::: :::	111
649	GCGAGCGAGAGGÁCCCGGA	671
111	InAspProAlaProPheLeuAsnArgLeuV	124
672	GAAGGCCGTCATCCTCGGCCACAGCTTCGGCGGCATGGTC	721
124 722	alargProArgArgSerAlaProLysGlyArgLysThrArgAlaArgArg 1	140 765
141	laileAlaAlaHisTyrGluValHisProArgProGlyGl	154
766	GCCTCGTCCTGGTCGCG	791
155	AspGlyAlaGln	158
792	CCTGGAGCCGGTGCGC	341
159	YThrValSer	166
842	CTGGCCACGCGAGCCATGT	891
167	erSerProLeuArgTyrAsnA 	183
892	GCTTCGAGAGCGCCATCGTGAACTTCCCGTCGCCGGCCGTGTTCGGGC	941
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233	laAlaSerSerLeuGlyProGlnLeuArgLeuCys	245
1059	CCCCAAGATGGGCAGCTTCGCGGCGCC	1108
246	alSerGlyLeuLeuAlaLeuArgProGlySerSerLeuArgIleA -::	262
0	AGCGGGGTC	1143
262	gThrLeuProTrpAlaHisLeuLysAlaAlaProPheLeuThrTyrP;	278

heGly 279

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seq_documentation_block:
ID AAV69289 standard; cDNA; 2832
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                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA sequence codes for murine JNK-interacting protein 1 (JIF-1, see AAWB1625), a novel cytoplasmic anchor protein that specifically binds to and inhibits the biological effects of JNK (c-Jun NH2-terminal kinase), including the initiation of apoptosis and oncogenic transformation. To isolate the clone, a yeast two-hybrid method was used to screen a mouse embryo cDNA library to identify proteins that interact with JNK. 7 Overlapping partial clones were isolated, and the full-length cDNA was subsequently . Obtained by screening a mouse brain lambda ZAPII cDNA hibrary. The invention provides JIP-1 nucleic acids and polypeptides, expression vectors and host cells. The JIP-1 polypeptide and nucleic acids (including antisense and ribozyme molecules) can be used in the manufacture of a medicament for treating a pathological condition associated with abnormal expression or activity of JNK, such as a neurodegenerative disease (selected from Parkinson's disease and Alzheimer's disease), a blood clot, stroke, malignancy, leukaemia, an autoimmune disease or inflammation (all claimed).
                     Percent Similarity:
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GTCTCGATCATCCTCCCCTCTGAAGACAGGAGAACAG

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:AAD25519

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alignment_block:
US-09-245-198A-4 x
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                                                                                                                                                                                                                                                                                                   CC bound to an aggregated protein-polycationic polymer conjugate or consisting in expression vector contains a promoter polynucleotide contigen which is a fragment of a gene or genome associated with an consisting of bacterium, fungus, protozoa and virus such as human cc immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C virus (HCV), influenza and respiratory syncytial virus (RSV), and coptionally comprising a nucleotide sequence encoding a cytokine expression vector), is useful for inducing an immune response (systemic and/or mucosal) in an organism. The cytokine expression vector (GW-CSF) or interleukin-12 (IL-12). The polymucleotide sequences encoding different promoter polymucleotide sequences. The cytokine contains a sequence for granulocyte macrophage-colony stimulating factor (different promoter polymucleotide sequences. The polymucleotide sequence encoding the antigen and the cytokine are under transcriptional control of same or CC present sequence is human herpesvirus 2 complete DNA genome related
                                                                                                                                                   Ratio:
Percent Similarity:
                                                                 Align seg 1/1 to reverse of: AAD25519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 90-132; 145pp; English.
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AAA09686 standard;
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                                                                                                                                                                                                                                                                                                                     This invention relates to an immediate early herpes-simplex-virus type 2 (HSV-2) infected cell protein 4 (ICP4) recognised by human cytotoxic T cells. HSV-2 ICP4 protein is recognized by cytotoxic T-lymphocyte (CTL) cells in humans and is used in vaccines for therapeutically or prophylactically treating HSV infections. Pharmaceutical compositions of HSV-2 ICP4 protein may be used to treat patients suffering from HSV infections, to prevent or decrease recurrent herpes disease, frequency, severity and duration of episodes. The present sequence represents HSV-2 DNA encoding ICP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immediate early herpes-simplex-virus type 2 (HSV-2) ICP4 protein is used in vaccines for therapeutically or prophylactically treating HSV infections -
                                                                                                                                                                                                                                                                                           Sequence
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vaccine; infection; ds.
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Human herpesvirus 2 c
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Human herpesvirus 2;
KW Human herpesvirus 2;
KW antiarthritic; rheuman
KW antiarthritic; yasc
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                                                                              Composition for oral delivery of vaccines, comprises expression vector containing antigenic genomic sequence, bound to aggregated protein-polycationic polymer conjugate or suspension -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnArgArgGlyArgArgGly......GluProGlyTh 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaGlnGluProAlaGlnGluGluLeuValAlaGluGluAspGlnAspPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rAlaLeuLeuValProLeuAlaLeuGlyLeuGlyLeuAlaLeuAlaCysL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....GCT 2225
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Disclosure; Page 90-132;

145pp; English

Sequence 154746 BP;

23003 A; 54218 C;

54701 G; 22824 T; 0 other;

to the invention.

different promoter polynucleotide sequences. The expression vector, as a DNA vaccine is useful for treating a condition in an organism. The present sequence is human herpesvirus 2 complete DNA genome related

Consisting a nucleotide sequence encoding an cytokine expression vector), is useful virus (HSV), hepatitis C virus (HSV), influenza and respiratory syncytial virus (HSV), influenza and respiratory syncytial virus (HSV), influenza and respiratory syncytial virus (HSV), and coptionally comprising a nucleotide sequence encoding an consisting of bacterium, fungus, protozoa and virus such as human communodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C virus (HCV), influenza and respiratory syncytial virus (RSV), and coptionally comprising a nucleotide sequence encoding a cytokine (or a cytokine expression vector), is useful for inducing an immune response contains a sequence for granulocyte macrophage-colony stimulating factor (GM-CSF) or interleukin-12 (II-12). The polynucleotide sequences encoding the antigen and the cytokine are under transcriptional control of same or different promoter interleukinear and control of same or different promoters.

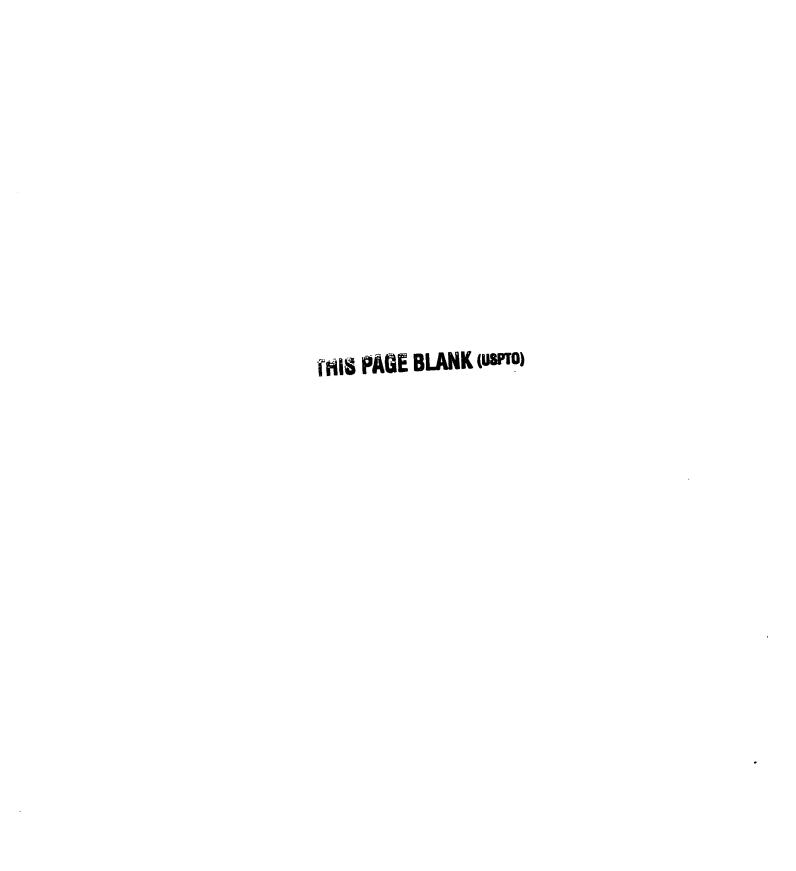
invention relates to a composition comprising an expression vector

alignment_block: US-09-245-198A-4 x AAD25519 alignment_scores: Quality: Align seg 1/1 to: AAD25519 Percent Similarity: 151813 GTGCGCGACGCGCTGGTGCTGATGCGCCTGCGCGGGGACCTGCGCGTGGC 151862 151716 GCCCGCCGCGCCCCGCGCGCGCGCGCGCCCGCCCGC 151762 152017 CTGGC......CGACACCGTCGCCGCGGCCGACTCGCTCGCCGCGCC 151985 TGCTCTTCCAGAACCA.....GAGCCTGCGCCCCCTG 151935 GCCGCGGAGCCCGCCGCTGCTGAGCTCCGCCGCCGCCGCCGCCGCGGACC 151932 151913 CCGG...... 151863 CGGCGGCAGGGCCGCCGTGGCCGCGTGCGCGCGTGAGCCTGGTCG 151763 CGCACGCCGACGCCCCGCCTGCGCGCGCGCGAGCTGCGGTTC 151812 103 oSerGluLeuAsnProGlnThrGluGluSerGlnAspProAlaProPheL 120 137 ArgAlaArgArgAlaIleAlaAlaHisTyrGluValHisProArgProGl 153 87 70 euGlyLeuLeuAlaValValSerLeuGlySerArgAlaSerLeuSer 86 53 rAlaLeuLeuValProLeuAlaLeuGlyLeuGlyLeuAlaLeuAlaCysL 70 26 aValArgGlnAlaGlnProProAlaProMetAlaAlaArg..... 10 AlaArgArgLeuProLeuProArgSerLeuGlySerArgAspGlyGlyAl 26 euAsnArgLeuValArgProArgArgSerAlaProLysGlyArgLysThr 136 AlaGlnGluProAlaGlnGluGluLeuValAlaGluGluAspGlnAspPr 103ArgSer 41 Ratio: 124.00 1.610 45.029 from: 1 to: 154746 Length: 171
Gaps: 8
Percent Identity: 30.409 . GGCCCTGGGCCCGGC..... 39 152057 152016 151984 151912 151931

152058 CGCCTCCGCGCGCGGGAGGCGCGCAAGCGCAA...GAGCCCCGCCCCGG 152104

152105 CCAGGGGGGCGCC 152117

153 yGlnAspGlyAla 157



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gb_pr:AF055872
gb_pr:BC019047
                                      gb_ba:SC6G10
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gb_htg:AP003911
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gb_htg:AP003634
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9b_ba:SCM10
9b_ba:SCM1
9b_pr:CNSOLDV6
9b_pr:ACO16708
9b_pr:ACO46708
9b_pr:HSBABDI1
9b_ba:AVINIFC
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9b_htg: AC105470

1b_ba: AF002222

1b_ba: AE004651

9b_ba: AE004740
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gb_ba:SGDNASTRS
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gb_ba:SC1C2
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gb_pat:AX180714
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Database length: 1873333701
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-Q-/cgn2_1/USPTO_spool/US09245198/runat_21062002_184006_9945/app_query.fasta_1.632
-Q-/cgn2_1/USPTO_spool/US09245198/runat_21062002_184006_9945/app_query.fasta_1.632
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXY=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXY=7.000 -START=1 -MATRIX=blosum62 -TRANS=hunan40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSITE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09245198_@CGN1_1_10697
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -MARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1
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                                          4.8e+03
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6.3e-18
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| AF030100 Mus musculus TWEAK mH
| AF030100 Mus musculus TWEAK mH
| 188 | AC016876 Homo sapiens clone
| 183 | AC069459 Mus musculus chrome
| 184 | AL603707 Mouse DNA sequence
| 185 | AL603707 Mouse DNA sequence
| 186 | AC098923 Rattus norvegicus of
| 186 | AC098923 
                             | AF002222 Pseudomonas aeruginos | AF002222 Pseudomonas aeruginos | AE004461 Pseudomonas aeruginos | AE004740 Pseudomonas aeruginos | AE04740 Pseudomonas aeruginos | AE04740 Pseudomonas aeruginos | AE04740 Pseudomonas aeruginos | AL1356595 Streptomyces coelicos | AL139164 Streptomyces coelicos | AL133425 Streptomyces coelicos | AL133425 Human chromosome | AC016708 Homo sapiens BAC clos | AL133425 Human chromosome | AC016708 Homo sapiens BAC clos | AL133455 Human chromosome | AL133475 Coryza sativa chromosome | AL031371 Streptomyces coelicos | AP003517 Oryza sativa chromosome | AL031371 Streptomyces coelicos | AP003511 Oryza sativa chromosome | AL031596 Human DNA sequence 
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i AF055872 Homo sapiens Apo3/DR:
i BC019047 Homo sapiens, Similar
i AF030099 Homo sapiens TWEAK mi
i AF140407 Sequence 1 from pater
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gb_ba:AE004731
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gb_ro:MMAF003115
gb_ro:AF054611
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US-09-245-198A-4 x AX201324
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                                                                                                                                                                                   AlaProPheLeuAsnArgLeuValArgProArgArgSerAlaProLysG1 133
                                                                          spGlnAspProSerGluLeuAsnProGlnThrGluGluSerGlnAspPro
                                                            ACCAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCT
                                                                                                                        ATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTGGCAGAGGAGG
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Ratio: 5.097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1353)
Ashkenazi A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
443 c 389 g 26
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66 ! AE003979 Oryza sativa chr
1 AF003115 Mus musculus JIP-1
1 AF054611 Mus musculus JNK i
1 ! AB070956 Streptomyces aver
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KEYWORDS
SOURCE
ORGANISM
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LOCUS AF055872
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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Homo sapiens Apo3/DR3 ligand
AF055872
AF055872.1 GI:3108230
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1368)
Marsters, S. A., Sheridan, J.P., Pitti, R.M., Brush, J., Ashkenazi, A.
                                                                                                                                                  Submitted (25-MAR-1998) South San Francisco, CA
                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                         2 (bases 1 to 1368)
Marsters, S.A., Sheridan, J.P., Pitti, R.M.,
                                                                                                                                                                                                                                            98228355
                                                                                                                                                                                                 Ashkenazi,A.
                                                                                                                                                                                                                                                                                   Identification of a ligand
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                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                         Biol. 8 (9),
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58. .807
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1. .1368
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94080, USA
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JOURNAL MEDLINE REFERENCE AUTHORS

FEATURES

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TITLE JOURNAL

REFERENCE AUTHORS

TITLE

ACCESSION VERSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gGlnIleGlyGluPheIleValThrArgAlaGlyLeuTyrTyrLeuTyrC
                                                                                                                                                                                                                             CCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATC
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                                                       CCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTACT
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Ratio: 5.097
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/product="Apo3/DR3 ligand"
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YYLYCQVHFDEGKAVYLKLDLLYDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL
RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH"
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REFERENCE
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KEYWORDS
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LOCUS BC019047
                                                                                                             FEATURES
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cyapbs-remail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCU19047

Homo sapiens, Similar to tumor necrosis superfamily, member 12, clone MGC:20669
                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLLL at: http://image.llnl.gov Series: IRAL Plate: 30 Row: p Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507596.
                                                                                                                                                                                                                                                                                                                                                                                           Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1651)
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C
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                                                                                                                                                                                                                                                                                                                                                                                  Web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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/clone_lib="NIH_MGC_48"
                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                http://www.nisc.nih.gov/
                    from
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factor (ligand)
IMAGE:4766071,
                    Tonsils"
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key,J.C.,
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Ratio: 4.842
milarity: 77.247
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GAGCCAAGATTTGAACCCAGCTAGAATGTGCCTGTGTACTGGACATGGTC
                                                         GCAGATGGAGGTTACACAACTTGTCTGAGGCCATGAGATACTAAGTGGTG
                                                                                                                      TCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGGAGCGCAG
                                                                                                                                                                               GCCTCGCAGAAGTGCACCTAAAGGCCGGAAAAACACGGGCTCGAAGAGCGA
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/protein_id="AAH19047.1"
/protein_id="AAH19047.1"
/db_xref="GI:17512139"
/translation="MAAARSQRRRGEPGTALLVPLALGLGLALACLGLLLAVVSL
GSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR
ARRAIAAHYEVHPPRGQDGAQADGGYTTCLRP"
1 517 c 481 g 309 t
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REFERENCE
AUTHORS
TITLE
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ACCESSION
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LOCUS AF030099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_pr:AF030099
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ORGANISM
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                                                                                                                                                                                                    that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
98070415
                                                                                                                                                                                                                                             Chicheportiche,Y., Bourdon,P.R., Xu,H., Hsu,Y.M., Scott,H., Hession,C., Garcia,I. and Browning,J.L.
TWEAK, a new secreted ligand in the tumor necrosis factor f
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens TWEAK mRNA, AF030099
                                                                                                                               Submitted (14-OCT-1997) Cell Biology, Cambridge, MA 02142, USA
                                                                                                                                                             Bourdon, P., Hession, C., Tizard, R. and Browning, J. Direct Submission
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1306)
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alignment_block:
US-09-245-198A-4 x
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Ratio: 5.110
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a 434 c 368 g 257 t
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Quality: 1265.00
Ratio: 5.080
Percent Similarity: 100.000
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LOCUS AR140407
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AR140407
AR140407.1 GI:14482903
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Location/Qualifiers
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Sequence 1 from Patent W00145730
AXI80714
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                                                                                                                                                                                                                                                                                                                                                 artificial sequence.
1 (bases 1 to 898)
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                                                                                                                                                                                                                 /note="human TWEAK fusion protein construct"
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Length: Gaps:

Percent Similarity:

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                                                                                                        seq_documentation_block:
LOCUS AF030100
DEFINITION Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1168)
Chicheportiche, Y., Bourdon, P.R., Xu, H., Hsu, Y.M., Scott, H.,
                                                                                               Mus musculus TWEAK mRNA, AF030100
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Ratio:
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TWEAK, a new secreted ligand in the tumor necrosis factor family
that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
98070415
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Chicheportiche, Y., Bixler, S.,
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                                                                                                                                                                                                                                                                                     Submitted (08-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 3, 2001 this sequence version replaced gi:13431059. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome, clone RP11-186B7 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC016876 190358 bp DNA linear HTG 03-SEP-2001 Homo sapiens clone RP11-186B7, WORKING DRAFT SEQUENCE, 16 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC016876
AC016876.4 GI:15421989
HTG; HTGS_PHASE1; HTGS_1
                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center project name: L3849
center clone name: 186_B_7
center clone name: 186_B_7
sequencing vector: M13; M77815; 3% of
Sequencing vector: Plasmid; n/a; 97% of
                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                  Center code: WIBR
                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
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Eutheria;
                                                                                                                                                                                                                                                 Genome Center
                                                                                                                      Project Information
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
  3% of reads
97% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604
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  misc_feature
                                               misc_feature
                                                                                                                                                                                                                                                                                                                                            misc_feature
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NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved
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Consensus quality: 181928 bases at least Q40
Consensus quality: 18529 bases at least Q30
Consensus quality: 187335 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102565 102664: gap of 100 bp
102665 116764: contig of 14100 bp in length
116765 116804: gap of 100 bp
116865 136408: contig of 19544 bp in length
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Insert size: 188858; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye;
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                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
22036. .24202
                                                                                                                                                                                                                                                                                                                                                           vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                       clone_end:SP6
                                                                                                                                                                                                                                               24303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-186B7"
                                                                 /note="assembly_fragment"
                                                                                                              /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40745: contig of 5624 bp in length
40845: gap of 100 bp
47136: contig of 6291 bp in length
47236: gap of 100 bp
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-u: gap of
180631: cr
1731
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190358: contig of 9627
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contig of 3897 b
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alignment_block:
US-09-245-198A-4 x AC016876/rev
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ORIGIN
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Percent Similarity:
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260 rgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPheLeuThr
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                                                                                                                                                                                  alTyrLeuLysLeuAspLeuLeuValAspGlyValLeuAlaLeuArgCys 226
                                                                                                                                                                                                                                ACTCGGCCTGTTGTCCCCACCCCAGGTGCACTTTGATGAGGGGAAGGCTG 83026
                                                                                                                                                                                                                                                                                                                                                                GGGTAACGCAGTAAGAGAGTGGCGAAGGGTTTGCCAGGAGAGTGGGGGAC 83176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGGTGTGGACGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAG 83326
                                                              gLeuCysGlnValSerGlyLeuLeuAlaLeuArgProGlySerSerLeuA 260
                                                                                                                                                                 TCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGCCCTGCGCTGC
                                                                                                                                                                                                                                                               .....ValHisPheAspGluGlyLysAlaV 210
                                                                                                                                                                                                                                                                                               GGGCTGGGCTCTACTACCTGTACTGTCAGGTAAGCCCCCATCTGGCTGCAT 83226
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4.679
65.625
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136509. 156380
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68265. .94625
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48605 c 50635 q
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Percent Identity:
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TITLE
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AUTHORS
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AUTHORS
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
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Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
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Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
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Murny, D. M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Worley, K., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrPheGlyLeuPheGlnValHis 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (31-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 25, 2001 this sequence version replaced q1:12621364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, 7 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                     NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 203083)
                                                                                                                                                                                                                                                                                                                                             Chémistry: Dye-primer Bodipy: 48% of reads chemistry: Dye-terminator Big Dye: 52% of reads Assembly program: phrap; version 0.990329 Consensus quality: 212648 bases at least Q40 Consensus quality: 218902 bases at least Q30 Consensus quality: 223384 bases at least Q30 Estimated insert size: 210056; sum-of-contigs estimation quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 7.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: MAFO
Center clone name: RP23-168P5
----- Summary Statistics
Sequencing vector: M13; L08821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- Project Information
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available and the accession
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alignment_block:
US-09-245-198A-4 x AC069459/rev
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GlyProGlnLeuArgLeuCysGlnValSerGlyLeuLeuAlaLeuArgPr
                                                                                                                                  euAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rSerSerProLeuArgTyrAsnArgGlnIleGlyGluPheIleValThrA 192
                                                                                                                                                                                        pGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAspGlyValL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCAGCCCTCTGCGCTACGACCGCCAGATTGGGGGAATTTACAGTCATCA 43206
                                                         GGGCCCCAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCC
                                                                                                                                                                            TGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAACGGTGTGC
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/chromosome="11"
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62252: 1
118772:
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Percent Identity: 64.444
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gap of unknown length
contig of 18207 bp in length
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42806

159 AlaGlyValAspGlyThrValSerGlyTrpGluGluAlaArgIleAsnSe 175

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alignment_block:
US-09-245-198A-4 x AL603707/rev
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AUTHORS
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Align seg 1/1 to reverse of: AL603707
                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           humqueryesanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 20, 2001 this sequence version replaced gi:16605765.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Ems. EMBL; Sw:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP: Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 234182)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by the group of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-422L16 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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VECTOR: pBACe3.6
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                                                                                                                                    555.50
4.553
67.778
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/note="Sequence from uni-directional primer reads and dGTP big dye terminator reads only."
1 56824 c 57519 g 60529 t
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AUTHORS
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12 (bases 1 to 179030)

13 (bases 1 to 179030)

14 (bases 1 to 179030)

15 (bases 1 to 179030)

16 (bases 1 to 179030)

17 (bases 1 to 179030)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC098923.4 GI:17973852
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus clone CH230-154B15, *** SEQUENCING ***, 68 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC098923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norway rat.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                      (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_dafa.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 68 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                  as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 179030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 137096 bases at least Q40 Consensus quality: 145080 bases at least Q30 Consensus quality: 152950 bases at least Q20 Estimated insert size: 138980; sum-of-contigs estimation quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: GIOK
Center clone name: CH230-154B15
Center clone summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Phrap; version 0.990329First
                                                                                                                                         7468
7568
12116
12216
20314
20414
     25590
25690
31435
31535
37596
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12115:
12215:
12313:
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gap of unknown contig of 8098 kgap of unknown contig of 5176 kgap of unknown contig of 5745 kgap of unknown contig of 6061 kgap of unknown contig of 6061 kgap of unknown
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length
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42773 4272; concity of 4477 by in length
42273 42234; concity of 3925 by in length
46235 46335 concity of 3925 by in length
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58006 50005; contig of 4272 by in length
58006 50005; contig of 4272 by in length
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58006 52800 spap of windown length
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58006 52800 spap of sold by in length
64468 68495; spap of windown length
64496 68495; spap of windown length
64497 77402 contig of 3921 bp in length
64496 68495; spap of windown length
64496 68496; contig of 3921 bp in length
64496 68496; contig of 3921 bp in length
64497 77402 contig of 3920 bp in length
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LOCUS AP002482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         following:GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakleabr.affrc.90.jp. URL:http://www.dna.affrc.90.jp:82/, Tel:81-298-38-7441, Fax:81-298-38-7468)
Fax:81-298-38-7468)
The orientation of the sequence is from T7 to SP6 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTN2.0, BLASTN2.0 as well as general to the content of the content of the sequence is from T7 to SP6 of the PAC clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Only in DataBase (2000) In press 2 (bases 1 to 187835)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T., Matsumoto,T. and Yamamoto, Oryza sativa nipponbare(GA3) genomic clone:P0706B05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-JUN-2000) Takuji Sasaki, National Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP002482.1 GI:8468009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detailed information on overlap and assembly quality together with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrhartoideae;
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                                                                                                                                                                                                                                                                                                                                                                                                               /clon
1765.
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/db_xref="G1:8468010"
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/translation="MASIQSGGDAAANGVDADVDGAASFPSAKRPRAGAGAAAITDAE
VRAEFAHHDRAVARLNNGTFGCCPASVLAARAKWQRLFLSQPDAFYFHHLQPGLARSR
ARVAAAVGAGDASEVSLVDNVTTAAAIIMQHVAWSFAEGDFARGDVVLMFLYTYCSIK
                                                                                                                                                                                                                                                                                                                                                   /www.similar to Streptomyces clavuligerus isopenicillinepimerase (P18549)"
                          ALRDAVAKLVADGFTCRKLRPPEKVH"
join(6984. .7174,7451. .7576,7735.
                                                                            GLRTMLRKQFKVEVPLYYNSKAAAADAPPEMVKDGNGDPVTGYVR1SHQVYNVREEYE
                                                                                                   AVAF THTRKDDPVSSKLHHPVVSSEYGNGLPMESAWTGVRDYSAQLVVPDVVDFVNRF
DGGVEGTRRNHDKVVEMGTMLAAAWGTFLGTPPEMCGSMLMVGLPGSLGVGSEDDAV
                                                                                                                                                     NSTHAYVARAGATVVEVPLPFPVSSPDATVAEFRAALAVARDGGRRRVRLAVTDHTTA
MPTVLTPVKELVATCREEGVDKVFVDAAHAVGQVPVDVRDTGADFYASNLHKWFFCPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4530"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ∕organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .187835
                                                                                                                                                                                                                                                                                                                                                                                                                                       Lone="P0706B05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryzeae; Oryza.
"hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187835 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
ne 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear PL clone: P0706B05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone: P0706B05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLN 10-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
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EKYNKELKSAYKSGVREGLAAGLGMGTVWULLFGGYSLGIWYGAKUILLKGYTGAKWI
NVIFAVLTGSIALGOASPSMKAFAGGOAAYKWFETINKKETIOAYSTTGMKPDDIRG
DIEFRDVYFSYPTRPDEQIFRGFSLSIPSGTTVALVGOSGSGKSTVISLIERFYDPOL
GDVLLDGVNLKGFQLRWIRSKIGLVSQDEVLFAASIKENIAYGKNATDQEIRAAAEL
ANASKFIDKNPOGLDTSVGEHGTOLSGGOKORIAIARAILADRRILLLDEATSALDAE
SERIVOEALDRVMTNRTTVIVAHRLSTVRNADTIAVIGOGILVEKGPHHELLKDPEGA
YSQLLKLQEANRQDKSDRKGDSGARSGKOLSINOSASRSRSSRNSHSTSVPGOMP
LGIDIQDGSSDNLCDGMPQDVPLSRLASLNKEPEIPVLLIGSIASVISGVIFPIFAILL
SNVIKAFYEPPHLLRKDSQFWSSMELVGAAVFLSLPVSSYLFSIAGCRLIKRIRLMT
FEKVVNMEIEWFDHPENSSGAIGARLSADAAKVBGLVGDALQLVVQNTTTLAGLVIA
FVSNWELSLIILALIPLIGLNGWIOMKETIGGFSADAKMYEEASQVANDAVSSIRTVV
SFSAEEKVMDLYKKKCEGPLRTGIRTGIISGIGFGVSFLLFGVYAASFVAGARLVEE
NKTTFPKVFVLALAMAAIGVSQSSTLTSDSSKAKSAVSSIFATVDRKSRIDPSEDA
GVTVETLHGNIEFGHYSFRYPTRDVEIFRDLGLTIHSGKTVALVGESGSGKSTAISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MPESWRDAEANASSSASVAAADSSPGNGKGGGGGGAAVARGER
AASASAARVPEHKLEAFADKTDAALMALGTLGAVANGAALPENTVLEGNLIDAEGGA
MGIHDVVNEWSIGETYLAIASAVASFVQVTCWHITGERQAARIRNLYLKTILRQL
IAFFDKYTNTGEVVGRNSGDTVLIQDANGEKVGKFIQLVVTFLGGFIVAFAQGHLITL
VMMATIPPLVVAGAVMSNVVAKMASLGQAAYAESSVVVEQTIGSIRTVASFTGEKQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(27285. .27309,29006. 29539. .29601))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Translation="MQYCVAVVRYARNVANVSSSRKQPCGRSIDVVTLMKTITINNLSP
LRPDETSCVDPHGIASRGDRDGRRDHVTRARABHGCMERKREISRRERRERVIRSLR
TQVVSHWIDLRIHWEGDYYYYLHEHERVISRVGYEVPPTALTDYFTTCPSSFLLIVIR
ILSGDLLIVFRCHINSHHSAPLVVIESIGRNSEVNARMQFY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAHTHRVGACVRVSARGRVSAQRDSGAARCDAVPDGAIGQPCVT SELFYSYRKHSKIIKFFCPNRGDLPAGGNLOGDREIVHETHTSN" join(19104. 19259, 19684. 19745, 19879. 20015, 20087. .2014 21463. .21598, 24585. .24645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQRFYDPDVGHILLDGVDIQKFQLKWLRQQMGLVSQEPALFNDTVRANIAYGKEGEAT
ESEIIEAAKLANAHKFISSSHQGYGTTVGERGAQLSGGQKQRIAIARAIVKDPKILLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVAREASRFSIAMVAMAIDDCAEQSWCFLVTKKHLLFFWI"
complement(join(8422 ...8775,8875...9168,9
                                                                                                                                                                                                                                                            complement(30314. .31296)
/note="3' LTR"
                                                                                                                                                                                                                                                                                                                            /translation="mtraasyHlntssStagClaawlRgGRICQRwSRDEQAaSSSIE
AMDPLASAGGAMKLKGKKGKEIKNLCSSKSCAPVEASRRWPTRKM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAA96613.1"
/db_xref="GI:8468013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTLMNIKDGAYASLVALHSAASS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEATSALDAESERVVQDALDRVMVNRTTVIVAHRLSTIQNADLIAVVKNGVIIEKGKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAA96612.1"
/db_xref="GI:8468012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F14M4 ; putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(8422. .8775, 8875. .9166,9253. .9516,
9642. .9908,9986. .1030,10934. .11207,11317. .11385
12632. .12870,12993. .13214,13312. .11487,11585. .139
/note="Similar to Arabidopsis thaliana chromosome 2,
/translation="mpedtavragesrprprypersvHLLsfamagLIppfsrffHev
LDfYEIHaLHLaPNAVMTLAIfvHLCemfIgrsTawLaVsDLGeeyDAVrDrLrgLrN
                                                                   /protein_id="BAA96616.1"
/db_xref="GI:8468016"
                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA96615.1"
/db_xref="GI:8468015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA96614.1"
/db_xref="GI:8468014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(16079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MVVFFFAHPIHGRTHDNNFSTPGVATEGGWGGSSGGKSMMADAE
IDRSRRRARRPRRPEIADGYLDPSQASRLYSIGFGSNFPNQILEGKYTPICAFSQRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="BAA96611.1"
/db_xref="GI:8468011"
                                                                                                                                                                                    /note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                          join(31975.
                                                                                                                                                                                                                                                        LTR"
                                                                                                                                                                                                                          .32199,32416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .16164,17463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABC transporter (AC004411)"
                                                                                                                                                                                                                          .32620,32656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .17646)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .29087,29375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .20015,20087. .20140,
                                                                                                                                                                                                                          .33163,33648. .33771)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13981))
2, BAC
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SRWDPPLCSDRDRESILAVMTVVGAGRGRSRRSGAGGGGDGTGSSGATAGGGRNGGSS

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alignment_block:
                                                                                                        alignment_scores:
                                            Percent Similarity:
                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                  Quality:
                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA96618.1"
/db_xref="G1:8468018"
/db_xref="G1:8468018"
/translation="MLAGSDDHRAGPRRGRGHCRRRVGEKMRRMPPRDARERKRQPHM
DFVVPSLWWPEMIVLEFVLAESSGRHAKLRRGRGLLEDRNDGKSLSVGSQTNTRRNVN
GDITKNSTMSSTLPPPIRPDKIVFSSLWFGGPPDEAWLRGGEGLVSAWAYNLALSTWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHVIPFAYYPFMAVAIIGAPPVPKTGARIMTQCVEDDHLPAFKEEIKAFDK" complement(57466. .57918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(54260. .54721)
/note="ESTs_AU031727(R0930),D24036(R0930) correspond to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GADGVADRLRAAAAPELSFTAAKTKETTTVAVGAAAARRSLRQPPRHPEHLSGFEGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAKAYLILGYSIESIRSLYLSPSPTFVPRSQNRVLVQRGIDVANESRKNNKKTWDPHV
SYTKNYKKRWASGGAEGGRWVQRPGDKGQLAAAQRGGGGMSGAWCPACAANPLPPAAA
HRRFSLALPPVADPNALPLLSLPPVGRRALPLLSRRSVGRGPVAAETRERRRWRAGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(41162..41301,41962..42181,44317..44345,44535..44778,46639..46732,47583..47695))
//note="hypothetical protein"
                                          145.50
0.983
47.134
                                                                                                                                                                     Similar to Nicotiana tabacum mRNA for HSR201 protein; hypersensitivity-related gene (X95343)"
                                                                                                                                                                                                                               complement(57466. .57918)
/note="EST AU032068(R3431) corresponds to a region of
                                                                                                                                                                                                                                                                                               /translation="mAGAAAWPAPAAGGNGGNGFYGNCFYPVSVVAESGAVEAADVAG
VVGMIREAKARLPADFARWAVADFREDPYELSFTYDSLFVSDWTRLGFLEADYGWGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSGGGGDRDRRGRLAVGRKKTGHQNGRVLATLGPATALSSTVLHALSAGHDAPASAVL
PPRPRTCKGRLRLATATRVGIPSKMAASGGGFFCTCGGGGVEGGRSGAGGGGGAAADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TMRRRPGVAPSPSTPGAATNDDEEEEEEAARSGATSADNKAARSVAAAIVVICFRCELM
CSLWKASVYILGAAGSNIVFMAVLSDSVVLAVHRINSDGTGASRFSEFNAQMSAIARL
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/translation="MLITTIDRVNRVHCRFIDLLGEPHLATMOHGOQVSIRKIRVDY
VAERRPAICWLDFFERFVGWILDWMRERAAAGSVTSGGTTATANEERPRPCPALPPPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(40163. .41147)
/note="5' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probably inactive because stop codons and positions are included in CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGDGSRAPGPNRGPGGDSASDPKGKRKMSEFGPPSPPHGGGAERTADRPPAGHKCPAA
SGVGRKKKRLRKIGQTEPCRGSFIEPPKWTFKRPPRRDRPLGSPSGTSDEESGSEGGG
                                                                                                                                            hypersensitivity-related gene/codon_start=1
                                                                                                                                                                                                        predicted gene.
                                                                                                                                                                                                                                                                                                                                            /protein_id="BAA96619.1"
/db_xref="GI:8468019"
                                                                                                                                                                                                                                                                                                                                                                                                                            region of the predicted gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQYRHISATSAKPPSKTAEGVKLHRFQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>AADDISMPAVGWCGWWWCERNGERRDMDSSLPLPPPLKLPLAAIASALARRRSLPADG</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGRRAEPADNDVTTRVLGGICMHTAWSSSPYCVSIVSFTVGYNIRCEKEEQRVPVEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /pseudo
34607^34613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal stop codon:complement36927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(34469. .36351,36628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDDWDDVVSGAGLGGLGTP"
                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HHHAAPCCLRPNQARETPADRHKSSFFFILSYTGQGRPLGIEDGKNKGWHDRLVCVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="one bp frameshift deletion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="one bp
35779~35794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="one bp
34922^34925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AB030283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Similar to Oryza sativa GAG-POL precursor
                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                          Percent Identity:
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                                                                                                      spGlyValLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAla 235
                                                                                                                                                            CTCTCTTTTTTTAACTTGATCGGGGCTCTCCTGTAGTGAGATTCCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Notes: Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC.

Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.

Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                      jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the mo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission
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Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
1 (bases 1 to 4210)
Murphy, L. and Harris, D.
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                                                               upstream initiation codon
                            IMPORTANT: This sequence MAY NOT be the entire insert of the
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It may be shorter because we only sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid IC2 lies between 8D9 and 7Al on the AseI-B genomic restriction fragment.
                                                                                                                                                                                                                                                                                                  1537. .1668
/gene="SC1C2.02"
/note="SC1C2.02, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tuberculosis) (543 aa), fasta scores; opt: 1753 z-score: 2214.2 E(): 0, 65.1% identity in 407 aa overlap, and pur2_HUMAN delta-1-pyrroline-5-carboxylate dehydrogenase (563 aa), fasta scores; opt: 1273 z-score: 1730.4 E(): 0, 48.5% identity in 408 aa overlap. Contains PS00687 and PS00070 Aldehyde dehydrogenases glutamic acid active site and cysteine active site and pfam match to entry PF00171 aldedh, Aldehyde dehydrogenases, score 114.70, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 active site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dehydrogenases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dehydrogenase, partial CDS, le
e.g. TR:O50443 (EMBL:AL010186)
                                                                                                                                                  /product="hypothetical protein
/protein_id="CAA19969.1"
/db_xref="GI:3355669"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="possible RBS
1537. .1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC1C2.01"
/note="PS00687 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KETLVAPTDYTYPHMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECTDPENEVFRTEYFGPFLAVHVYDDSADDAYDAMLTQMESVSDYALTGSVISNDRAA
AAYTMEKLRYAAGNFYINDKSTGAVVGQQPFGGGRASGTNDKAGAPQNLMRWTLTRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TMGDVTDLSNFIGAVIDERSFAKNKAAIDRAKEDETCTIVAGGSYDDSVGYFVRPTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Translation="IDSPCELIDEWRENVHYARNILAEOPPANSQGVWNRMDHRPLEG
FYAAITEFNISAIAANILITAPALMGNVVWKPSPTQTHAAVLLMQLLEEAGLPKOVIK
LUTGDGIAVSEVALEHDLAGIHFTGSTKTROHLMKTYGNUTEKYRTY PELVGETGK
DELVAHPSADRAVLKTALTRGAFEYQGQKCSATSRAYIPASIWNDGFKEEFAAEVDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="delta-1-pyrroline-5-carboxylate dehydrogenase"
/protein_id="CAA19966.1"
/db_xref="G1:3355668"
/db_xref="SPTREMBL:086502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8e-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     delta-1-pyrroline-5-carboxylate dehydrogenase
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/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC1C2.01"
/note="PS00070 Aldehyde dehydrogenases cysteine active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Pfam match to entry PF00171 aldedh, Aldehyde
dehydrogenases, score 114.70, E-value 1.8e-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=2
/transl_table=11
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/note="SC1C2.01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC1C2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1246. .1283
/note="hairpin_loop with 18bp stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SC1C2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="true overlap with cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="cosmid 1C2"
                                                                                                                      /db_xref="SPTREMBL:086503"
                                                                                                                                                                                                                                            transl_table=11
                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                                        /gene="SC1C2.02"
L537. .1668
                                                                                         translation="MAETTVRRRVRHLSRTSDSDRKNAAAALQRSLDRRDNGGATGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1189
                                                            . 2787
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                                                                                                                                                                                                                                                                                                            questionable
                                                                                                                                                                                                                                                                                                                                                                                                                                                               upstream of SC1C2.02*
                                                                                                                                                                                                                                                                                                               ORF,
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alignment_scores:
    Quality:
                            alignment_block:
US-09-245-198A-4 x
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Percent Similarity:
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  SC1C2/rev
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3052. .4140
/gene="ilvE"
                                                                                                                                                                                                                /gene="SC1C2.05c"
complement(4214..5644)
/gene="SC1C2.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCIC2.04, ilvE, probable branched-chain amino acid aminotransferase, len: 362 aa: similar to many, e.g. ILVE_BACSU putative branched-chain amino acid aminotransferase (362 aa), fasta scores; opt: 1047 z-score: 1401.5 E(): 0, 44.7% identity in 360 aa overlap. Contains PS00770 Aminotransferases class-IV signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SCIC2.03, leuB, probable 3-isopropylmalate dehydrogenase, len: 347 aa; similar to e.g. LEU3_CORGL 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (340 aa), fasta scores; opt: 1450 z-score: 1318.1 E(): 0, 68.0% identity in 338 aa overlap. Contains PS00470 Isocitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:086505"
/translation="MTTPTIELKPSAHPLSDSERAAILANPGFGRHFTDHMVTIKWTE
GRGWHDGQLVPYAPLSLDPATMVLHYAQEIFEGLKAYRRPDGSVATFRPEKNGARFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="branched-chain amino
/protein id="CAA19971.1"
/db_xref="GI:3355671"
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                                                                                                                                                                                                                                                                                                                                                                                                            LGYEAEEGRVSVDQWQRDSENGTLTEVFACGTAAVITPVGTVKRAGAQWQQSGGETGE
VTQRLRDALLDIQRGTVADPHGWMHTLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSRRLGMPELPVDTFIEACDALVAQDEKWVPAHGGEESLYLRPFMIATEVGLGVRPAN
EYLFIVIASPAGAYFPGGVKPVSIWVSEDRVRAVPGGMGDAKTGGNYAASLLAQAEAA
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LRPSKLLPGVATPLAGQPEIDFVVVREGTEGPYTGNGGTIRKGTEHEVATEVSVNTAY
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/transl_table=1
/product="3-isopropylmalate dehydrogenase"
/protein_id="cAA19970.1"
/db_xref="GI:3355670"
                                                                                                                                                                                                                                                                                                    complement(4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKGCDQVCYLDAIERKWVEELGGMNLYFVYGNKIVTPSLTGSILEGVTRDSLLTVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="leuB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEIGDTLAARVAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHGSAPDIAGQGKADPTATVLSVALLLRHLGYEDEAARIEDAVSADLGERGDLPARST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAATIFLVTDPARFDVIVTDNLFGDIITDLAAAVSGGIGVAASGNINPSGDFPSMFEP
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                                                                                                     140.00
0.828
                                                                                                                                                                                                                                                                                                                        /note="PS00770 Aminotransferases class-IV signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="possible RBS upstream of ilvE'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PS00470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="leuB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MSRSLNLAVIPGDGIGQEVVAEGLKVLSAVLPQDVKLETKEFDF/
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                                                                                 50.448
                                                                           Percent Identity: 28.358
                                                                                                                                                                                                                                                           2.05c"
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Align seg 1/1
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8960 CAGGCGGCGCCCCTGGCGTCGGTCCGGCCGCAGGATCTCCAGGTACA 8911
                                                                                               9010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9680 GGAACTCGCCGCGAGATGCCCTCGGCGAGCAGGGCGGTCAGGTCGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9630 TGCCAGGCGCCTCGATGGCGGCCTGCCGGTCGCGGGCCTCGTCGGGGGC 9581
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                                          ...ThrAlaAlaSerSerLeuGlyProGlnLeuArgLeuCysGlnValSe
                                                                                                                                                                                         CGACGCCGCTTGCACACGTAGTGGTTGATGTAGGAGTAGTCGGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCCATGTCCACTCCCGGGTCTTCTAGGTCCTCGGCTGTTGCTGCGTGA 9190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uAspGlnAspProSerGlu.LeuAsnProGlnThrGluGluSerGlnAsp 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGGCCGTCGGGGACGTACAGGTCGACGTAGGCGCCGAGGCGTTCGCGG 9481
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                                                                                                                                                                                                                                                                                                                                   IleValThrArgAlaGlyLeuTyrTyrLeuTyrCysGlnValHisPheAs 205
                                                                                                                                                                                                                                                                                                                                                                                  GTCACCGTCCGCGCGAACAGGCGGCGGAAGATGCCCGCGGCGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                               er...SerProLeuArgTyrAsnArg......GlnIleGlyGluPhe 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerGlnArgArg.ArgGlyArgArgGlyGluProGlyThrAlaLeuLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCAGTGGATGCCCCCCCCCCCCCCACCCGAAGATCGTACGCGCGTCCACCAGG 9140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...GCCGCCATGGTGAGCTTCTCCAGCCCGCGCTCGGCGATCATCTCCAT 9290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCGCTCCACTCCAGGGTGCGCAGCAGCAGTTCGTCCTTGGAGCCGAAGT 9381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuSerAlaGlnGluProAlaGlnGluGluLeuVal.....AlaGluGl 99
                                                                                            TCGCCCTCCTCCTTCAGGACGGTCGGGGCGGCACCTCGACGACCTC 8961
                                                                                                                                         euAlaLeuArgCysLeuGluGluPheSerAla.....
                                                                                                                                                                                                                                    pGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAspGlyValL 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ly...AlaValArgGlnAlaGlnProProAlaProMetAlaAlaArgArg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .GlyValAspGlyThrValSerGlyTrpGluGluAlaArgIleAsnSerS 176
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TITLE
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REFERENCE
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AUTHORS
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ORGANISM
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LOCUS AL646059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Blologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Pondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex Christian, Boucher@toulouse.inra.fr
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2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salanoubat, M., Genin, S., Artiguenave, F., Gouzy, J., Mangenot, S., Arlat, M., Billault, A., Brottier, P., Camus, J.C., Cattolico, L., Chandler, M., Cholsne, M., Claudel-Renard, C., Cunnac, S., Demange, N., Gaspin, C., Lavie, M., Moisan, A., Robert, C., Saurin, W., Schiex, T., Siguier, P., Thebault, P., Whalen, M., Wincker, P., Levy, M., Weissenbach, J. and Boucher, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ralstonia solanacearum.
Ralstonia solanacearum
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segment 3/19.
AL646059 AL646052
AL646059.1 GI:17427391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the plant pathogen Ralstonia solanacearum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://sequence.toulouse.inra.fr/R.solanacearum.html.
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Gene name confidence: hypo
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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AAQHIYGYAIGLDMTRRDLQNAAKKGGRPWETGKAFDGSAPIGPIVPAQTVASPDRGA
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alignment_block:
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                                         Similarity:
                                                                                Quality:
                                                             Ratio:
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Gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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Gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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PROTEIN"
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Align seg 1/1 to reverse of: AL646059
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205 AspGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAspGlyVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCCGAGCCGATGATGATGGCCGAGGCCGCGCGCGCTACAACGTCGAGCGC
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                                                                                                                                                                                                            GACGGTCGCGCGCATCGCGCAGGAAGCCGGCATCAGCATGCTGACCGTGC 129341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGTGCAACGTGGCGGCCGGCTCGGCCCTGCTGCAGAACGAGCCGCTGG 129491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rgArgAlaIleAlaAlaHisTyrGluValHisProArgProGlyGlnAsp 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oArgArgSerAlaProLysGlyArg.....LysThrArgAlaA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCGAGGTCGAGCCGAT......CGCCGTGCAGATCGCCG 129635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrGluGluSerGlnAspProAlaProPheLeuAsnArgLeuValArgPr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGCAAGCGGCTGGGCGCCCGGCTATGCGGTCTCGGAGATGGTGGCGTCC 129720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACATCGCACCGGATGCGCCGCCGCATAGCTTGTGCACAACATTTAGGC 129970
                                                                    ACGGCCGCACCCGCCGACTTGTACCAC.....
                                                                                                                                                                                                                                                                         rSerProLeuArgTyrAsnArgGlnIleGlyGluPheIleVal.....
                                                                                                                                                                                                                                                                                                                                             GTCACGCTCAAGATCCGCACCGGCTGGGACCGCGAGCACCGCAACGCGCT 129391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGC.....GCAGATCATCGACATCAACATGGGCTGCCCGGCCAAGAA 129541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProAlaGln.....
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                                                                                                                                    .....ThrArgAlaGlyLeuTyrTyrLeuTyrCysGlnValHisPhe
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ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTCAAGGCCTCGGTGCGCATCCCGGTGGTCGCCAACGGCGACATCGGCA 129233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sAlaAlaProPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davis, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Eukaryota; Metazoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC105470 233912 bp DNA linear Rattus norvegicus chromosome Rf1 clone CH230-192N7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC105470.2 GI:18158251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
Worley, K., Wu, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 233912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
   Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129183
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WORKING DRAFT
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JOURNAL
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     findPhrapList
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 224207 bases at least Q40 consensus quality: 227463 bases at least Q30 consensus quality: 229761 bases at least Q30 Estimated insert size: 217555; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 6.6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid; M77789

Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329First call to
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Center clone name: CH230-192N7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project Information
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of 1003
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of 1960
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of 8589
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of 26851 bp in
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alignment_block:
US-09-245-198A-4 x AC105470/rev
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ORIGIN
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Ratio: 0.916
Percent Similarity: 47.452
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                                                                                                                                                                             32325 GGTCGAGCCTAGCCCTGGGGCAGCGGCCCCCCGCGACTCCGGCGGGGTCTG 32276
                                                                                                                                                                                                                                                                       32363 GAGAACGGACACGAGGCCGCCCCG.....AAGGCGAGGCCCC 32326
                                                                                                                                                                                                                                                                                                                                                                            94 luLeuValAlaGluGluAspGlnAspProSerGluLeuAsnProGlnThr 110
:: ||| |||:::||| ||| ||| ::: |||
32404 AC.....GCGGCTGAGGAGCCAG...CCCATGGAGACGACGGGCGCCCACC 32364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32448 GCC.....GCTCGTTGCAGGAGCCGCTGCGGCCTGGCCGACCATGTCGG 32405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32498 GCGGTGGGCGGAGCTCGGGGAGTGCCGCGGGCCCTGACGCACTGTCGTC 32449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32524 CGGCGAGGTGAGCGGCCCGGGC.................CTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32624 AGGGTCTGTGGACCCGGACAAGCCCTAGGGGGGTCCGAGTGTGACCGCGG 32575
                                                                                                                       143 AlaAlaHisTyrGluValHisProArgProGlyGlnAspGlyAlaGlnAl 159
                                                                                                                                                                                                          127 rgArgSerAlaProLysGly...ArgLysThrArgAlaArgArgAlaIle 142
                                                                                                                                                                                                                                                                                                                             111 GluGluSerGlnAsp.ProAlaProPheLeuAsnArgLeuValArgProA 127.
159 aGlyValAspGlyThrValSerGlyTrpGluGluAlaArgIleAsnSerS 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 yLeu.GlyLeuAlaLeuAla...CysLeuGlyLeuLeuLeuAlaValVal 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 ArgArgGlyGlu...ProGlyThrAlaLeuLeuValProLeuAlaLeuGl 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 laGlnProProAlaProMetAlaAlaArgArgSerGlnArgArgArgGly 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 SerLeuGlySerArg.AlaSerLeuSerAlaGlnGluProAlaGlnGluG 94
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/db_xref="taxon:10116"
/chromosome="Rf1"
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1. .233912
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227588: gap of unknown length
228852: contig of 1264 bp in length
228952: gap of unknown length
229963: contig of 1011 bp in length
230063: gap of unknown length
231343: contig of 1280 bp in length
231443: gap of unknown length
231443: gap of unknown length
232645: contig of 1202 bp in length
232745: gap of unknown length
232745: gap of unknown length
232745: gap of unknown length
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Gaps: 24
Percent Identity: 31.210
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	erGlyLeuLeuAlaLeuArgProGlySerSerLeu 259	248
31889	AAGCGGCGGATCGCGAATCGGGCCGCGAGGGCTGCGTCTGTGCTGCGTAG	31938
248	AlaSerSerLeuGlyProGlnLeuArgLeuCysGlnValS	235
31939	TGCTTAGGCTACAGCGGGCCTGCGGGCGGGCGGCCCCGGAAGAGGAA 31939	31985
234	CysLeuGluGluPheSerAlaThrAla	226
31986	32032 GGAGTTTGTGGGGTCGACTTTGAGGCCGACCCGGGCTGCTCGCGCGG	32032
225		210
32033	32082 GGCGCGCTCGCCGGCCGGGCCCGGGCGCGGTCACGCGCCTTTGAGTTTGCA	32082
209	Ala	209
32083	TTGGCGCCACGCGGCGGGGGGGGGGGGGGGGGGCCGGCGGAACAGTGCCT	32132
208		200
32133	TGCGGCCCCAGGCCGCCGGCCGCCTTTGTTCCGGGGCAGTCTTTTG	32182
200		193
32183	CAACGCCAGCAAGAACGAGGAGGACGCGGGGTAGG	32217
192		176
32218	32237 GGCGCCGAAGGCGACCAGAT 32218	32237

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Result
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BI766766 603056866F1 NIH_MGC_122 BI766766.1 BI766766 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens mRNA sequence. GI:15758344 834 bp mRNA linear EST 25-SEP-2001 Homo sapiens cDNA clone IMAGE:5206217 5',

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

numan.

RESULT BI766766 LOCUS

ALIGNMENTS

DEFINITION

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 834)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

REFERENCE AUTHORS TITLE

COMMENT

JOURNAL

Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can

þe

found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11517 row: c column: 18 High quality sequence stop: 772.

Location/Qualifiers . 834

FEATURES

source

/INDIFFUSATION / INDIFFUSATION /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5206217" /lab_host="DH10B" /clone_lib="NIH_MGC_122"

pcmv-sport6;

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                                                                                                                                     ccacagtcgtcacaggctgccggctcccctcgacagctctctgggcacccggtcccc-tc
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11437 row: 1 column: 03
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini;
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/db_xref="taxon:9606"
/clone="ITMAGE:5175698"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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Query Match 55.8 Best Local Similarity 98.0 Matches 818; Conservative

RESULT 2
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BI819200 603034614F1

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                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM12034 row: b column: 07
                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 731)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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603395825F1 NIH_MGC_90
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                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        numan
                                               125
                                         /organism="Homo sapiens"
/db_xref="Maxon:9606"
/db_xref="Maxon:9606"
/clone=_lib="NAH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage resistant)"
/note="organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
25 a 242 c 228 g 136 t
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603243254F1 NII
mRNA sequence.
BI596681
Eukaryota; Metazoa; Chordata; Cri
Mammalia; Eutheria; Primates; Cai
1 (bases 1 to 828)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mc
Unpublished (1999)
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                                                       Craniata; Vo
Catarrhini;
                 Mammalian
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420

548

300

428 180 368 120

240

360



Query Match

51.1%;

Score

701

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DΒ 10;

Length

731;

COMMENT

Strausberg, Ph.D

Gene

Collection

Euteleostomi;

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659 848 599 788 540 728

IMAGE:5285892

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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
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/clone="IMAGE:5285892"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
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Pred. No. 4.6e-122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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/clone_lib="NIH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

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     Dept of m
                  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave
                                                             Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hilller,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Carden,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
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1 (bases 1 to 1027)

Cousin,P., Billotte,J., Chaubert,P. and Shaw,P.H.

Physical map of 17p13 and the genes adjacent to p53

Genomics 63 (1), 60-68 (2000)
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Institute of Pathology
Rue du Bugnon 25, Lausanne, VD 10
sub_clone=AB2R Asc-BamHI PSI1180
Class: BAC subclone.
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/db_xref="taxon:9606"
/map="17p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Human"
317 c 282 g
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Best Local Similarity
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EST.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10019 row: e column: 18
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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1 (bases 1 to 910)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Location/Qualifiers
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/db_xref="taxon.9606"
/clone="IMAGE:4367225"
/clone=lib="NIH_MGC_86"
/clone_lib="NIH_MGC_86"
/tissue_type="osteosarcoma, cell line"
/tasue_type="osteosarcoma, 
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603038693F1 NIH_MGC_115
                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11447 row: j column: 23
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
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Location/Qualifiers
            /note-"Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source annonymous pool of male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library is
                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179510"
/clone_lib="NIH_MGC_115"
                                                                    /lab_host="DH10B"
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primed and
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IMAGE:5179510 5',
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Tissue Procurement: Jeffréy E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution informations of the control of th
                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                     Email: cgapbs-r@mail.nih.gov
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/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1:
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1:
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                                              Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN (Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                        URL:http://genome.gsc.riken.go.jp/, Fax:81-45-503-9216)
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Please visit
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/dev_stage="adult"
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                         Unpublished (1997)
Other_ESTs: ur70d09.x1
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National Cancer Institute, Cancer Genome Ana
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Mammalia; Eutheria;
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561 bp mRNA linear EST 04-MAY-20 ur70d09.yl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3155633 5' similar to TR:054907 O54907 TNF-RELATED WEAK INDUCER OF APOPTOSIS
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h quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="129 - C57/B6 - FVBN"
/db_xref="taxon:10090"
/clone="IMAGE:3155633"
/clone_iib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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158 c 194 g 100 t 1 others
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BG686319.1 GI:13917716
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Contact: Robert Strausberg, Ph.D
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
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1 (bases 1 to 587)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DHIOB (phage-resistant)"
/note="organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4766071"
/clone_lib="NIH_MGC_48"
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Pred. No. 4.6e-75;
0; Mismatches 2;
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Catarrhini; Hominidae;
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  Query Match
Best Local Similarity
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Library was constructed by Dr. Douglas Melton DNA sequencing
Washington University Genome Sequencing Center For informatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
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456 bp mRNA linear EST 23-OCT-21 ie72g04.yl Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA 5' similar to TR:043508 043508 TNF-RELATED WEAK INDUCER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Other_ESTs: ie72g04.x1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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(bases 1 to 456)
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                                                                                                           57
                                                                                                                                                               made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from Library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated
                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
                                                                                                                                                by hydroxyapatite chromatography and
                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Both"
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  32.1%;
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  Score 440.2; DB 1
Pred. No. 1.4e-74;
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Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,J., Cardenas
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                                                                                                                        Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by Washington University Genome Sequencing Center For information
                                                                                                                                                                                                                                                     Harvard University, Howard Hughes Medical Dept of Molecular and Cellular Biology, 7
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                                                                                                                                                                                                                                                                                                                  Contact: Douglas Melton, Klaus H.
                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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                                                                                                    obtaining a clone please contact: Juliana
                                                                                                                                                                                          Fax: 617-495-8557
                                                                                                                                                                                                             Tel: 617-495-1812
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                                                                              (brown@fas.harvard.edu)
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                                                             quality sequence stop: 415
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/organism="Homo sapiens"
                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:17122611
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Human Islet 4 N4-HIS 1
O54907 TNF-RELATED WEAK
                                                                                                                                                                                                                                                                                                                  Kaestner,
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                                                                                                         Brown
                                                                                                                                                                                                                                                  Institute
Divinity Ave,
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Homo sapiens EST 27-NOV-2001

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299

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Cambridge,

by:

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Search completed: June
Job time: 18070 sec
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ORIGIN
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Best Local Sim
Matches 438;
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                                                                                                                                                                                                                                                                                                                                                                                                              CCBCBTABBATACAGTATLCCCACTCTTATCTTACAACTCCCCCCACCGCCCACCTCTCCCACC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCTCCCCTCGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCTCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cggctcccctcgacagctctctgggcacccggtcccctctgccccaccctcagccgctct 950
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                                                                                                                                                                                                                                                                                                                                    CCACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCTCCACC 300
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Similarity 99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    þ
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186 c
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/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex-"Both"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                    22, 2002, 10:49:15
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Pred. No. 6.3e-74;
0; Mismatches 2; Indels 0;
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